



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102152

TO: John Ulm
Location: CM-1/10D19
Art Unit: 1646
Wednesday, August 27, 2003
Case Serial Number: 09988745

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Ulm,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954



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SEARCH REQUEST FORM

Access DB# 102152

OL 8/26

RECEIVED Scientific and Technical Information Center

Requester's Full Name: AUG 22 1988 41m Examiner #: 69507 Date: 8-22-87
 Art Unit: 1646 Phone Number: 308-4008 Serial Number: 09/988745
 Mail Box and Bldg/Room Location: CM1 Results Format Preferred (circle): PAPER DISK E-MAIL
10217

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

please send SEQ ID NO: 2 of
 09/988,745.
 reg 2 - 337 AN

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Type of Search		Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>8/26</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>8/27</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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QY 181 QMLEEMPCVSCOLLNKFWMGNLFPEVPCIMISLYKIFVATROAOQITTLSSKL 240
DB 181 QMLEEMPCVSCOLLNKFWMGNLPLFEVPCIMISLYKIFVATROAOQITTLSSKL 240
QY 241 AGAAKHEKRAKKTIGIYVGYLLCWLPTTIDTWDLSLHFTTPPLVDFITWFAVENSAC 300
DB 241 AGAAKHEKRAKKTIGIYVGYLLCWLPTTIDTWDLSLHFTTPPLVDFITWFAVENSAC 300
QY 301 NPIIYVESYQWFRKALKITLSQKVFSPQTRTVDLXOE 337
DB 301 NPIIYVESYQWFRKALKITLSQKVFSPQTRTVDLXOE 337

RESULT 2
US-10-225-567A-358
Sequence 358, Application US/10225567A
Publication No. US20030113796A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 358
LENGTH: 337
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-358

Query Match 100.0%; Score 1785; DB 15; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-153;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRAVFIGAEHHPAFCYQVNGSCPRVHTLGIQVLYITFCAGMLIIVGNFVAFAVS 60
DB 1 MRAVFIGAEHHPAFCYQVNGSCPRVHTLGIQVLYITFCAGMLIIVGNFVAFAVS 60
QY 61 YFKALHTPTNELLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLPFLCLT 120
DB 61 YFKALHTPTNELLALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLPFLCLT 120
QY 121 SIFHLCTSIDRHCAICDPLIYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERLS 180
DB 121 SIFHLCTSIDRHCAICDPLIYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERLS 180
QY 181 QMLEEMPCVSCOLLNKFWMGNLPLFEVPCIMISLYKIFVATROAOQITTLSSKL 240
DB 181 QMLEEMPCVSCOLLNKFWMGNLPLFEVPCIMISLYKIFVATROAOQITTLSSKL 240
QY 241 AGAAKHEKRAKKTIGIYVGYLLCWLPTTIDTWDLSLHFTTPPLVDFITWFAVENSAC 300
DB 241 AGAAKHEKRAKKTIGIYVGYLLCWLPTTIDTWDLSLHFTTPPLVDFITWFAVENSAC 300
QY 301 NPIIYVESYQWFRKALKITLSQKVFSPQTRTVDLXOE 337
DB 301 NPIIYVESYQWFRKALKITLSQKVFSPQTRTVDLXOE 337

RESULT 3
US-10-330-220-4
Sequence 4, Application US/10330220
Publication No. US20030113789A1
GENERAL INFORMATION:
APPLICANT: Wang et al.
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

;; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
;; FILE REFERENCE: CLO00755CON
;; CURRENT APPLICATION NUMBER: US/10/330,220
;; PRIOR FILING DATE: 2002-12-30
;; PRIOR APPLICATION NUMBER: US 09/637,603
;; PRIOR FILING DATE: 2000-08-15
;; PRIOR APPLICATION NUMBER: US 60/192,326
;; PRIOR FILING DATE: 2000-03-27
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 321
;; TYPE: PRT
;; ORGANISM: HOMO SAPIEN
US-10-330-220-4

Query Match 95.4%; Score 1703; DB 15; Length 321;
Best Local Similarity 100.0%; Pred. No. 4e-146;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 CYQVNGSCPRVHTLGIQVLYITFCAGMLIIVGNFVAFAVSYFKAHTPTNELLST 76
DB 1 CYQVNGSCPRVHTLGIQVLYITFCAGMLIIVGNFVAFAVSYFKAHTPTNELLST 60
QY 77 ALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLPFLCLTNSIFHLCTSIDRHCAI 136
DB 61 ALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDLPFLCLTNSIFHLCTSIDRHCAI 120
QY 137 CDPLIYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERLSQMLEEMPCVSCOLL 196
DB 121 CDPLIYPSKFTYRVALRYILAGWGPAAVTSFLYTDVVERLSQMLEEMPCVSCOLL 180
QY 197 NKEFGWLNPLFEVPCIMISLYKIFVATROAOQITTLSSLAGAAKHEKRAKKTIGI 256
DB 181 NKEFGWLNPLFEVPCIMISLYKIFVATROAOQITTLSSLAGAAKHEKRAKKTIGI 240
QY 257 VVGIIYLLCWLPTTIDTWDLSLHFTTPPLVDFITWFAVENSACNPIIYVESYQWFRKAL 316
DB 241 VVGIIYLLCWLPTTIDTWDLSLHFTTPPLVDFITWFAVENSACNPIIYVESYQWFRKAL 300
QY 317 KLTLSQKVFSPQTRTVDLXOE 337
DB 301 KLTLSQKVFSPQTRTVDLXOE 321

RESULT 4
US-10-251-852-5
Sequence 5, Application US/10251852
Publication No. US20030119144A1
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CLO00899-CON
CURRENT APPLICATION NUMBER: US/10/251,852
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 09/781,559
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: 09/694,821
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/208,929
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 321
TYPE: PRT
ORGANISM: Human
US-10-251-852-5
Query Match 95.4%; Score 1703; DB 15; Length 321;

Best Local Similarity 100.0%; Pred. No. 4e-146;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy	17	CYOVNSCCPRTVHTLGIOLVYLTCAGLLIVLGNVY,AVASFEKRLHPTEFLLSL	76
Db	1	CYOVNSCCPRTVHTLGIOLVYLTCAGLLIVLGNVY,AVASFEKRLHPTEFLLSL	60
Oy	77	ALADMEGLLVLP,LSIRSVESCFEGDFLCRLHYLDYI,FCLSIFHLCTSIDRHCAL	1368
Db	61	ALADMEGLLVLP,LSIRSVESCFEGDFLCRLHYLDYI,FCLSIFHLCTSIDRHCAL	1202
Oy	137	CDBLLYPSKFTYVVALRYILAGMGVPAAYTSLELYTDVYI,TRLSQLMEHPCVSCOLL	1968
Db	121	CDBLLYPSKFTYVVALRYILAGMGVPAAYTSLELYTDVYI,TRLSQLMEHPCVSCOLL	1802
Oy	197	NKRWGLNRPPLFVNPCLIMISLYKIFVATYQAQOITTY,SKSLAGAAKHEKRAKTLGI	2562
Db	181	NKRWGLNRPPLFVNPCLIMISLYKIFVATYQAQOITTY,SKSLAGAAKHEKRAKTLGI	2402
Oy	257	VWGIYLLCWL,PFIDIMNDSLHFTTPPLVPIFIWFYAYI,NSACNPIIYVSZYOMFKAL	3168
Db	241	VWGIYLLCWL,PFIDIMNDSLHFTTPPLVPIFIWFYAYI,NSACNPIIYVSZYOMFKAL	3002
Oy	317	KLTIISOKEVSPQRTVDLXOE	337
Db	301	KLTIISOKEVSPQRTVDLXOE	321

RESULT 5

US-10-225-567A-645
Sequence 645, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
TITLE OF INVENTION: ANTISENSE PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 645
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-645

Query Match	45.58;	Score 812.5;	DB 15;	Length 348;
Best Local Similarity	46.18;	Pred. No. 1.4e-65;		
Matches 152;	Conservative 64;	Mismatches 105;	Indels 9;	Gaps 3

[illegible]

Dd 254 RKAAKLTGLMAAEFLVSWLPYLVDADVAIDAYANFTTPPIYVEILWCYTYSANMPLIYA F 313

Q7 308 SYQWFRKALKLTLISQVRESFQRTIVDLIOE 337
 ||||| :||| : || : || :
Dd 314 FYQWFGKATKLIVSGNVLRTDSSSTINLPSE 343

RESULT 6

```

US-09-995-225-10
: Sequence 10, Application US/09995225
: Publication No. US20020193584A1
: GENERAL INFORMATION:
: APPLICANT: Chen, Ruoping
: APPLICANT: Chu, Zhi Liang
: APPLICANT: Dang, Huang T.
: APPLICANT: Lowitz, Kevin P.
: APPLICANT: Priddy, Cameron
: TITLE OF INVENTION: Endogenous And No. US70020193584A1-Endogenous Versions of Humane
: TITLE OF INVENTION: Receptors
: FILE REFERENCE: AREN-0308
: CURRENT APPLICATION NUMBER: US/09/995,225
: CURRENT FILING DATE: 2001-11-26
: PRIOR APPLICATION NUMBER: 09/170,496
: PRIOR FILING DATE: 1998-10-13
: PRIOR APPLICATION NUMBER: PCT/US99/23938
: PRIOR FILING DATE: 1998-10-13
: PRIOR APPLICATION NUMBER: 60/253,404
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/255,366
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: 60/270,286
: PRIOR FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/282,365
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/270,266
: PRIOR FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/282,032
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/282,358
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/282,356
: PRIOR FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: 60/290,917
: PRIOR FILING DATE: 2001-05-14
: PRIOR APPLICATION NUMBER: 60/309,208
: PRIOR FILING DATE: 2001-07-31
: NUMBER OF SEQ ID NOS: 67
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 10
: LENGTH: 345
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20020193584A1 Sequence
US-09-995-225-10

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Query Match	44.1%	Score 786.5	DB 10	Length 345
Best Local Similarity	44.2%	Pred. No. 3e-63		
Matches 146	Conservative 70	Mismatches 105	Indels 9	Gaps 3

[illegible]

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Db      194 VNQMWWLTDLSEFIPIFFIMILLGNIFLVARQAKIENTGSKTESSESSEYKARVARE 253
      248 RKAATIGIYVIGILCWLPTPTIDPMVDSLHFTPLPLVDFIIFMFAFNSACNPITVE 307
      254 RKAATIGVYVAVMISMLPISIDSLDAFMGFITPACIYETICMCATYNSANMPLIYAL 313
      308 SYOMFRRAKLTLSOKVESPQTRTVLDYXOE 337
      314 FYPMFRRAIKIVYTGVOVLKNSATMNLFE 343
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RESULT 7

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US-09-782-974C-84
; Sequence 84, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 41USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; PRIORITY FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/774,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-84
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Query Match      44.1%: Score 786.5; DB 11; Length 345;
Best Local Similarity 44.2%: Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;
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QY      17 CY-OVNSCPRVTWTGIGQIYLYLTCAAGMLIIVGNVFAFAVSFKALHTPTNPLLS 75
      14 CYANVNSCVKIPSPGSRVILYVFGGANLVAFGNLWVMSILHKKQLHSPNPLVAS 73
      76 LALADMFLGLIYVPLSTIRSVSCWFGDFLCRLHTYLDLFLCLTSIFHLCFISIDRCA 135
      74 LACADFVLGVYVMPFSWVRVESCWYFGRSFCFPHCCDVAFCYSSLFHLCFISIDRYIA 133
      136 ICDDLPKSKFTVVALRYTLAGWGPAAVTSLSFLYTDVETRSLQMLEEPCVGSQOL 195
      134 VTDDPLVPTRKFTVSVSGICISVSWILPLMTSGAVFYGVDDGLEELSDALNCTGGCQTV 193
      196 LNKFMGLNFPPLVPCILMISLYVKIFVAVTRQAOOI-TTLLSKS-----LAGAAKHE 247
      194 VNQMWWLTDLSEFIPIFFIMILLGNIFLVARQAKIENTGSKTESSESSEYKARVARE 253
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QY      248 RKAATIGIYVIGILCWLPTPTIDPMVDSLHFTPLPLVDFIIFMFAFNSACNPITVE 307
      254 RKAATIGVYVAVMISMLPISIDSLDAFMGFITPACIYETICMCATYNSANMPLIYAL 313
      308 SYOMFRRAKLTLSOKVESPQTRTVLDYXOE 337
      314 FYPMFRRAIKIVYTGVOVLKNSATMNLFE 343
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RESULT 8

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US-09-995-225-10
; Sequence 10, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Zhong Liang
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Endogenous And No. US20030139588A9- Endogenous Versions of Huma
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; PRIORITY FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCY/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-10
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Query Match      44.1%: Score 786.5; DB 12; Length 345;
Best Local Similarity 44.2%: Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;
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QY      17 CY-OVNSCPRVTWTGIGQIYLYLTCAAGMLIIVGNVFAFAVSFKALHTPTNPLLS 75
      14 CYANVNSCVKIPSPGSRVILYVFGGANLVAFGNLWVMSILHKKQLHSPNPLVAS 73
      76 LALADMFLGLIYVPLSTIRSVSCWFGDFLCRLHTYLDLFLCLTSIFHLCFISIDRCA 135
      74 LACADFVLGVYVMPFSWVRVESCWYFGRSFCFPHCCDVAFCYSSLFHLCFISIDRYIA 133
      136 ICDDLPKSKFTVVALRYTLAGWGPAAVTSLSFLYTDVETRSLQMLEEPCVGSQOL 195
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Db      134 VTDPLVPTKFTVSVSGICISVWIIPLMTSGAVETGVTDGLEELSDALNIGCCQY 193
QY      196 LNFKMGWLNPLFEVPCILMISLYKIFVATROAOI-TTLSKS-----LAGAAKHE 247
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      194 VNQNMVLTDFLSFFITFIMILYKNIPLVARQAKIEVTGSKTSSSSYKARVARE 253
QY      248 RKAATLGIVVGIYLLCMLPFTIDVDSILHFTTPPLVDFITWAFNSACNPIIYVF 307
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      254 RKAATLGIVVAVAFMISWLPYSIDSLDAWGFITPACIEICWCAYNSANPLIYAL 313
QY      308 SYOMFRKALKTLSOKVFSPOTRVDLYOE 337
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      314 FYPMFRKAIKIVITGVOLKNSSATMNLFSE 343

RESULT 9
US-10-225-567A-685
; Sequence 685, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 685
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-225-567A-685

Query Match      44.1%; Score 786.5; DB 15; Length 345;
Best Local Similarity 44.2%; Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY      17 CY-QVNGSCPRTVHTGIQIVITLCAAGMLIIVLGAVF/APAVSYFKALHTPTNELL 75
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      14 CYANVNGSCVKIIPFSGSRVILYIVGFGAVLAVFGML/MISILHKQLHSPTNPLVAS 73
QY      76 LADADFEGLVLPSTIRSVESQWFRGDFLCRLHTPLDPLFCLTSTFHLCFTSIDRHC 135
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      74 LACADFLVGVTVMPFSVNRVESCWFGRSFCFTHCCD/AFCTYSSLFHLCFTSIDRYIA 133
QY      136 ICDPLTPSKFTVVALRYILAGWVPAATSLFLYVDVETRLSQWLEMPGVSCQLL 195
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      134 VTDPLVPTKFTVSVSGICISVWIIPLMTSGAVETGVTDGLEELSDALNIGCCQY 193
QY      196 LNFKMGWLNPLFEVPCILMISLYKIFVATROAOI-TTLSKS-----LAGAAKHE 247
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      194 VNQNMVLTDFLSFFITFIMILYKNIPLVARQAKIEVTGSKTSSSSYKARVARE 253
QY      248 RKAATLGIVVGIYLLCMLPFTIDVDSILHFTTPPLVDFITWAFNSACNPIIYVF 307
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      254 RKAATLGIVVAVAFMISWLPYSIDSLDAWGFITPACIEICWCAYNSANPLIYAL 313
QY      308 SYOMFRKALKTLSOKVFSPOTRVDLYOE 337
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      314 FYPMFRKAIKIVITGVOLKNSSATMNLFSE 343

RESULT 10
US-10-251-852-2
; Sequence 2, Application US/10251852
; Publication No. US20030119144A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
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```

; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NOCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000899-CON
; CURRENT APPLICATION NUMBER: US/10/251,852
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 09/781,559
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 09/694,821
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/208,929
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Human
US-10-251-852-2

Query Match      44.1%; Score 786.5; DB 15; Length 345;
Best Local Similarity 44.2%; Pred. No. 3e-63;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY      17 CY-QVNGSCPRTVHTGIQIVITLCAAGMLIIVLGAVF/APAVSYFKALHTPTNELL 75
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      14 CYANVNGSCVKIIPFSGSRVILYIVGFGAVLAVFGML/MISILHKQLHSPTNPLVAS 73
QY      76 LADADFEGLVLPSTIRSVESQWFRGDFLCRLHTPLDPLFCLTSTFHLCFTSIDRHC 135
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      74 LACADFLVGVTVMPFSVNRVESCWFGRSFCFTHCCD/AFCTYSSLFHLCFTSIDRYIA 133
QY      136 ICDPLTPSKFTVVALRYILAGWVPAATSLFLYVDVETRLSQWLEMPGVSCQLL 195
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      134 VTDPLVPTKFTVSVSGICISVWIIPLMTSGAVETGVTDGLEELSDALNIGCCQY 193
QY      196 LNFKMGWLNPLFEVPCILMISLYKIFVATROAOI-TTLSKS-----LAGAAKHE 247
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      194 VNQNMVLTDFLSFFITFIMILYKNIPLVARQAKIEVTGSKTSSSSYKARVARE 253
QY      248 RKAATLGIVVGIYLLCMLPFTIDVDSILHFTTPPLVDFITWAFNSACNPIIYVF 307
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      254 RKAATLGIVVAVAFMISWLPYSIDSLDAWGFITPACIEICWCAYNSANPLIYAL 313
QY      308 SYOMFRKALKTLSOKVFSPOTRVDLYOE 337
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      314 FYPMFRKAIKIVITGVOLKNSSATMNLFSE 343

RESULT 11
US-09-995-225-14
; Sequence 14, Application US/09995225
; Publication No. US20020193584A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Huma
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
```

```
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,365
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/270,266
;; PRIOR FILING DATE: 2001-02-20
;; PRIOR APPLICATION NUMBER: 60/282,032
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,358
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/282,356
;; PRIOR FILING DATE: 2001-04-06
;; PRIOR APPLICATION NUMBER: 60/290,917
;; PRIOR FILING DATE: 2001-05-14
;; PRIOR APPLICATION NUMBER: 60/309,208
;; PRIOR FILING DATE: 2001-07-31
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 342
;; TYPE: PRF
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-14
```

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Query Match 44.0%; Score 785.5; DB 10; Length 342;
Best Local Similarity 43.9%; Pred. No. 3.7e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;
```

```
QY 17 CYQ-VNGSCPRTVTGIGQIVYITLCAAGMLIIVGNVFAVSYFKAHTPTNFIILS 75
  ||| ||||| : : : : : ||| : : : : : ||| : : : : : ||| ||||| :
DB 13 CYEVNNGSCITPTSPGSRVILYTAFFGSLAVFGNLLVMTSVLHKQLHSPNFIILAS 72
QY 76 LALADMFGLLVLPLSTIRSVESCMFEGDFLCRLHTYLDLFCILTSIFHLCFISIDRHA 135
  ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 73 LACADFLVGTVLMFMSVRVESCWFYGAKECTLHSCDVAFCYSVYLHCFICIDRYIV 132
QY 136 ICDPLLPKRTVVALRYIILAGGCVPAATYSLFLYDYVETRLSQMLEHPVCVGSQQL 195
  : ||| : : ||| : : : : : : : : : : : : : : : : : : : : : |||
DB 133 VTDPLVATKFTVSVSIGCISVSWILPLTVSGAVFYGVNDGIEELVSALNCVGGCOII 192
QY 196 LNKFMGLNPFLEFVPCILMISLVKIFVATROAOQITTLSSLAGA-----AKHE 247
  : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 193 VSQGWVLIDFLFFIPLVMIILSKIFLAKQAIRKIEITSSVSESSSEYKIRVAKRE 252
QY 248 RKAATIGIYVGIILCWLPEITDMVDSLHFTPLPVDFITWFAVFNACNPITIVF 307
  ||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 253 RKAATIGVTVLAVISWLPYTVDLIDAFMGFLTPAYIYICCMASVYNSAMNPLIYAL 312
QY 308 SYOWFRKAKLTLSQKVFSPQTRVVDLXOE 337
  - ||||| : : : : : : : : : : : : : : : : : : : : :
DB 313 FYWFRRAIKLILSGDVLKASSSTISLFE 342
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```
RESULT 12
US-09-791-932-118
;; Sequence 118, Application US/09791932
;; Publication No. US20030003451A1
;; GENERAL INFORMATION:
;; APPLICANT: Vogell, Gabriel
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Hiebsch, Ronald R.
;; APPLICANT: Lind, Peter
;; APPLICANT: Kayles, Paul S.
;; APPLICANT: Ruff, Valerie
;; APPLICANT: Huff, Rita M.
;; APPLICANT: Wood, Linda S.
;; TITLE OR INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referen
;; FILE REFERENCE: 00325, US1
;; CURRENT APPLICATION NUMBER: US/09/791,932
;; CURRENT FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/184,305
;; PRIOR FILING DATE: 2000-02-23
```

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;; PRIOR APPLICATION NUMBER: 60/184,304
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,303
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,397
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/184,247
;; PRIOR FILING DATE: 2000-02-23
;; PRIOR APPLICATION NUMBER: 60/188,880
;; PRIOR FILING DATE: 2000-03-13
;; PRIOR APPLICATION NUMBER: 60/217,369
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/217,370
;; PRIOR FILING DATE: 2000-07-11
;; PRIOR APPLICATION NUMBER: 60/218,492
;; PRIOR FILING DATE: 2000-07-20
;; PRIOR APPLICATION NUMBER: 60/186,810
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/188,064
;; PRIOR FILING DATE: 2000-03-09
;; PRIOR APPLICATION NUMBER: 60/186,457
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: 60/213,861
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: 60/194,344
;; PRIOR FILING DATE: 2000-04-03
;; PRIOR APPLICATION NUMBER: 60/218,337
;; PRIOR FILING DATE: 2000-07-14
;; NUMBER OF SEQ ID NOS: 184
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 118
;; LENGTH: 342
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-09-791-932-118
```

```
Query Match 44.0%; Score 785.5; DB 11; Length 342;
Best Local Similarity 43.9%; Pred. No. 3.7e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;
```

```
QY 17 CYQ-VNGSCPRTVTGIGQIVYITLCAAGMLIIVGNVFAVSYFKAHTPTNFIILS 75
  ||| ||||| : : : : : ||| : : : : : ||| : : : : : ||| ||||| :
DB 13 CYEVNNGSCITPTSPGSRVILYTAFFGSLAVFGNLLVMTSVLHKQLHSPNFIILAS 72
QY 76 LALADMFGLLVLPLSTIRSVESCMFEGDFLCRLHTYLDLFCILTSIFHLCFISIDRHA 135
  ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 73 LACADFLVGTVLMFMSVRVESCWFYGAKECTLHSCDVAFCYSVYLHCFICIDRYIV 132
QY 136 ICDPLLPKRTVVALRYIILAGGCVPAATYSLFLYDYVETRLSQMLEHPVCVGSQQL 195
  : ||| : : ||| : : : : : : : : : : : : : : : : : : : : : |||
DB 133 VTDPLVATKFTVSVSIGCISVSWILPLTVSGAVFYGVNDGIEELVSALNCVGGCOII 192
QY 196 LNKFMGLNPFLEFVPCILMISLVKIFVATROAOQITTLSSLAGA-----AKHE 247
  : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 193 VSQGWVLIDFLFFIPLVMIILSKIFLAKQAIRKIEITSSVSESSSEYKIRVAKRE 252
QY 248 RKAATIGIYVGIILCWLPEITDMVDSLHFTPLPVDFITWFAVFNACNPITIVF 307
  ||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
DB 253 RKAATIGVTVLAVISWLPYTVDLIDAFMGFLTPAYIYICCMASVYNSAMNPLIYAL 312
QY 308 SYOWFRKAKLTLSQKVFSPQTRVVDLXOE 337
  - ||||| : : : : : : : : : : : : : : : : : : : : :
DB 313 FYWFRRAIKLILSGDVLKASSSTISLFE 342
```

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RESULT 13
US-09-995-225-14
;; Sequence 14, Application US/09995225
;; Publication No. US20030139588A9
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Ruoping
;; APPLICANT: Chu, Zhi Liang
;; APPLICANT: Dang, Huang T.
```

```

1  APPLICANT: Lowitz, Kevin P.
2  APPLICANT: Pride, Cameron
3  TITLE OF INVENTION: Endogenous And No. US2003013958A9-Endogenous Versions Of Human C
4  TITLE OF INVENTION: Receptors
5  FILE REFERENCE: AREN-0308
6  CURRENT APPLICATION NUMBER: US/09/995,225
7  CURRENT FILING DATE: 2001-11-26
8  PRIOR APPLICATION NUMBER: 09/170,496
9  PRIOR FILING DATE: 1998-10-13
10 PRIOR APPLICATION NUMBER: PCT/US99/23938
11 PRIOR FILING DATE: 1998-10-13
12 PRIOR APPLICATION NUMBER: 60/253,404
13 PRIOR FILING DATE: 2000-11-27
14 PRIOR APPLICATION NUMBER: 60/255,366
15 PRIOR FILING DATE: 2000-12-12
16 PRIOR APPLICATION NUMBER: 60/270,286
17 PRIOR FILING DATE: 2001-02-20
18 PRIOR APPLICATION NUMBER: 60/282,365
19 PRIOR FILING DATE: 2001-04-06
20 PRIOR APPLICATION NUMBER: 60/270,266
21 PRIOR FILING DATE: 2001-02-20
22 PRIOR APPLICATION NUMBER: 60/282,032
23 PRIOR FILING DATE: 2001-04-06
24 PRIOR APPLICATION NUMBER: 60/282,358
25 PRIOR FILING DATE: 2001-04-06
26 PRIOR APPLICATION NUMBER: 60/282,356
27 PRIOR FILING DATE: 2001-04-06
28 PRIOR APPLICATION NUMBER: 60/290,917
29 PRIOR FILING DATE: 2001-05-14
30 PRIOR APPLICATION NUMBER: 60/309,208
31 PRIOR FILING DATE: 2001-07-31
32 NUMBER OF SEQ ID NOS: 67
33 SOFTWARE: PatentIn version 3.1
34 SEQ ID NO 14
35 LENGTH: 342
36 TYPE: PRT
37 ORGANISM: Artificial Sequence
38 FEATURE:
39 OTHER INFORMATION: No. US2003013958A9e1 Sequence
40 US-09-995-225-14

```

```

: Publication No.: US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenn C.
: APPLICANT: Roush, Christine L.
: TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: PRIOR APPLICATION NUMBER: 60/257,144
: PRIOR FILING DATE: 2000-12-19
: NUMBER OF SEQ ID NOS: 2292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 687
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-225-567A-687

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Query Match 43.98; Score 783.5; DB 15; Length 342;
Best Local Similarity 43.98; Pred. No. 5.6e-63;
Matches 145; Conservative 69; Mismatches 107; Indels 9; Gaps 2;

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OY 17 CYO-VNGSCPRVTHLGIOLVLYLCAAGMLIYLGAVFAVAFAYFKALHTPTNELLIS 75
   ||: ||||| |::|:::| |::| |::| |::| |::| |::| |::| |::| |
Db 13 CYEDVNGSCIEPTPSGSRVILYTAFSGLAVFGNLLVMTSVLHFKQLHSPTNELLIS 72
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
OY 76 LALADMFGLLVLPSTIRSVESCMFEGDFLCRLHTYLDLFCULTSIFHLCFISIDRCA 135
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
Db 73 LACADFLVGVTVMLFSWVRVVEGCMVFGAKFCTLHSCDDVAFGYSVLHLCFICIDRYIV 132
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
OY 136 ICDPLLPKSKFTVVALRYILAGWGVPAATYSLFLYDVETRLSQMLEMPCYGSCOLL 195
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
Db 133 VTDLVYATKFTVSAGCISVSWILPLTYSGAFTGVDNDGLELVSAINCVCGCCOI 192
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
OY 196 LNKFMGMLNFPPLFVPCIMISLVYKIPVATROAOITTLKSLAGA-----AKHE 247
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
Db 193 VSOGWVLIDFLFFLPILVMIILYSKIFLAKQAIIETTSKYESSSESKIRVAKRE 252
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
OY 248 RKAATIGIVVGIYLLCMLPPTIDMWDSLHFTYPPPLVFDIFTWFAVFNACNPDIYF 307
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
Db 253 RKAATIGVTVLAVVISWLPYTVDLIDAFMGFLTPAYIYEICWMSAYYNSAMNPLIYAL 312
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
OY 308 SYQWFRKAKLTLSQKVFSPQRTVDLXQE 337
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
Db 313 FYPMFRRAIKLILSGDVLKRASSSTISLFL 342
   ||: ||: |::|:::| |::| |::| |::| |::| |::| |::| |::| |
```

Search completed: August 26, 2003, 14:25:53
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2003, 14:21:02 ; Search time 44 Seconds
(without alignments)
1215.701 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785
Sequence: 1 MRAVFQGAEEHPAFCYGV.....LFLSQVFSPQRTVDLYOE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA1982.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA1997.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA2001.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseq-e-hbl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1785	100.0	337	18 AAM09110	Human amine recept
2	1785	100.0	337	20 AA13736	Human amine recept
3	1785	100.0	337	23 ABB78232	Amino acid sequenc
4	1785	100.0	337	24 ABB56910	Human orphan GPCR
5	1785	100.0	337	24 ABB99760	Amino acid sequenc
6	1785	100.0	337	24 ABB81936	Human putative neu
7	1703	95.4	331	22 AAG65596	Human putative neu
8	812.5	45.5	339	24 ABB37891	NOVA protein sequ
9	812.5	45.5	348	21 AAB18764	Amino acid sequenc

10	812.5	45.5	348	23 ABB98168	Human AXOR 106 aml
11	812.5	45.5	348	24 ABB81735	Human trace amine
12	795.5	44.6	338	21 AAB18765	Amino acid sequenc
13	786.5	44.1	345	22 AAG80970	Human nGPR40 #2.
14	786.5	44.1	345	23 ABB93788	Human G-protein-co
15	786.5	44.1	345	23 ABB52417	Human G-protein-co
16	786.5	44.1	345	23 ABB04072	Human G-protein co
17	786.5	44.1	345	23 AAU97600	Human G-protein co
18	786.5	44.1	345	24 ABB73007	Amino acid sequenc
19	785.5	44.0	342	22 ABB81756	Human trace amine
20	785.5	44.0	342	22 AAU25611	Human G-protein-co
21	785.5	44.0	342	22 ABB04074	Human G-protein co
22	785.5	44.0	342	23 AAU20086	Human G-protein co
23	785.5	44.0	342	24 ABB73040	Amino acid sequenc
24	785.5	44.0	342	24 ABB99740	Human trace amine
25	785.5	44.0	342	24 ABB81757	Human G-protein co
26	783.5	43.9	342	22 AAG65595	Human trace amine
27	735.5	41.2	351	23 ABB79888	Human G-protein co
28	724.5	40.6	332	23 AAE23417	Human SNORF66 orph
29	697.5	39.1	306	18 AAW35831	Human G-protein co
30	697.5	39.1	306	18 ABB98746	Human G-protein co
31	696.5	39.0	295	22 AAG72401	Human OR-1like poly
32	696.5	39.0	306	24 ABB57089	Human GPCR 58128 (
33	696.5	39.0	306	24 ABB81701	Human G-protein-co
34	686	38.4	319	22 AAG72332	Human G-protein-co
35	677.5	38.0	339	22 AAG80973	Human OR-1like poly
36	677.5	38.0	339	22 AAG80973	Human G-protein co
37	677.5	38.0	339	22 AAB49232	Human SNORF33 rece
38	677.5	38.0	339	23 ABB93791	Human G-protein-co
39	677.5	38.0	339	23 ABB04073	Human G-protein co
40	677.5	38.0	339	24 ABB81732	Human trace amine
41	674.5	37.8	343	19 AAW59907	Human HNHC132 (G-P
42	674.5	37.8	343	23 ABB81702	Human G-protein-co
43	670.5	37.6	339	24 ABB80694	Human trace amine
44	657	36.8	332	22 AAB49234	Mouse SNORF33 rece
45	626	35.1	332	23 ABB80695	Rat trace amine re

ALIGNMENTS

RESULT 1
AAW09110
ID AAW09110 standard; Protein; 337 AA.
XX
AC AAM09110:
XX
DT 05-APR-1997 (first entry)
XX
DE Human amine receptor.
XX
XX
KW Amino receptor; 7-transmembrane receptor; neurotransmitter;
KW signal transduction; therapy; diagnosis; agonist; antagonist.
XX
OS Homo sapiens.
XX
PN MO639440-AL.
XX
PD 12-DEC-1996.
XX
PF 06-JUN-1995; 95WO-US07221.
XX
PR 06-JUN-1995; 95WO-US07221.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI LI Y, Ruben SM;
XX
XX
DR WPI: 1997-043075/04.
XX
XX N-PSDB; AAT51051.
XX
XX DNA encoding human amine receptor - used to identify agonists and
PT antagonists, or amine neurotransmitters

XX Claim 8; Fig 1A-1C; 68pp; English.

PS A novel human mature 7-transmembrane receptor (hAR09110) was

CC putatively identified as an amine receptor (hAR) on the basis of

CC sequence homology to the rat amine receptor. Its amino acid

CC sequence was deduced from a cDNA clone (AA751051) obcd. from a human

CC genomic library. Recombinant mature hAR can be expressed in host

CC (e.g. E. coli, COS, insect) cells and used to raise antibodies, to

CC identify amine neurotransmitters transported by hAR, and to screen

CC for agonist/antagonist cpts. useful for treating conditions related

CC to hAR under-/over-expression.

XX Sequence 337 AA;

SQ

Query Match 100.0%; Score 1785; DB 18; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.5e-186;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVGNVFAFVAVS 60

DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVGNVFAFVAVS 60

QY 61 YFKALHPTNPLLSLALADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTFCLT 120

DB 61 YFKALHPTNPLLSLALADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTFCLT 120

QY 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

DB 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

QY 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

DB 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

QY 181 QMLEMPGVSCQLLNKFMGMNPLFEFVPCIMISLYKIFVAVRQAQOITLTSKSL 240

DB 181 QMLEMPGVSCQLLNKFMGMNPLFEFVPCIMISLYKIFVAVRQAQOITLTSKSL 240

QY 241 AGAAKHEKAKAKTIGIVGIYILCMLPTIDTMDSLHFTTPPLVPDIFIMFAVFNASAC 300

DB 241 AGAAKHEKAKAKTIGIVGIYILCMLPTIDTMDSLHFTTPPLVPDIFIMFAVFNASAC 300

QY 301 NPIIYVESYQWFRKALKLTLSQKVFSPQTRTVDLXQE 337

DB 301 NPIIYVESYQWFRKALKLTLSQKVFSPQTRTVDLXQE 337

RESULT 2

AAI13736

ID AAI13736 standard; Protein: 337 AA.

AC AAI13736;

DT 13-SEP-1999 (first entry)

XX Human amine receptor polypeptide.

DE Human amine receptor; recombinant.

XX Homo sapiens.

OS Homo sapiens.

XX US5928890-A.

PN US5928890-A.

XX 27-JUL-1999.

PD 27-JUL-1999.

XX 06-JUN-1995; 95US-0467559.

PF 06-JUN-1995; 95US-0467559.

PR 06-JUN-1995; 95US-0467559.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (HUMA-) HUMAN GENOME SCI INC.

XX L1 Y;

PI L1 Y;

XX WPI; 1999-429497/36.

DR N-PSDB; AAX81288.

XX

PT Human amine receptor polynucleotides, vectors and host cells

XX Claim 1; Fig 1; 22pp; English.

PS This sequence represents a human amine receptor polypeptide. Host cells

CC transformed with a vector comprising the amine receptor coding sequence

CC are used for the recombinant production of the polypeptide. The

CC polypeptides are useful for treating conditions related to under-

CC expression and over-expression of the human amine receptor.

XX Sequence 337 AA;

SQ

Query Match 100.0%; Score 1785; DB 20; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.5e-186;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVGNVFAFVAVS 60

DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVITLCAAGMLITVGNVFAFVAVS 60

QY 61 YFKALHPTNPLLSLALADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTFCLT 120

DB 61 YFKALHPTNPLLSLALADMFGLVPLSTIRSVESCFEGDFLCRLHTYLDLTFCLT 120

QY 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

DB 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

QY 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

DB 121 SIFHLCEISIDRHCACDPLLYPSKFTVVALRYILAGMGPAAVTSLEFYTDDVETRLS 180

QY 181 QMLEMPGVSCQLLNKFMGMNPLFEFVPCIMISLYKIFVAVRQAQOITLTSKSL 240

DB 181 QMLEMPGVSCQLLNKFMGMNPLFEFVPCIMISLYKIFVAVRQAQOITLTSKSL 240

QY 241 AGAAKHEKAKAKTIGIVGIYILCMLPTIDTMDSLHFTTPPLVPDIFIMFAVFNASAC 300

DB 241 AGAAKHEKAKAKTIGIVGIYILCMLPTIDTMDSLHFTTPPLVPDIFIMFAVFNASAC 300

QY 301 NPIIYVESYQWFRKALKLTLSQKVFSPQTRTVDLXQE 337

DB 301 NPIIYVESYQWFRKALKLTLSQKVFSPQTRTVDLXQE 337

RESULT 3

ABB78232

ID ABB78232 standard; Protein: 337 AA.

AC ABB78232;

DT 25-NOV-2002 (first entry)

XX Amino acid sequence of a human amine receptor.

DE Amino acid sequence of a human amine receptor.

XX Human; amine receptor; G-protein coupled receptor; receptor;

KW dopamine D2 receptor.

XX Homo sapiens.

OS Homo sapiens.

XX US2002086362-A1.

PN US2002086362-A1.

XX 04-JUL-2002.

PD 04-JUL-2002.

XX 20-NOV-2001; 2001US-0988745.

PF 20-NOV-2001; 2001US-0988745.

PR 06-JUN-1995; 95US-0467559.

PR 19-MAY-1999; 99US-0314006.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (HUMA-) HUMAN GENOME SCI INC.

XX L1 Y; Ruben SM;

PI L1 Y; Ruben SM;

XX WPI; 2002-635676/68.

DR N-PSDB; ABQ78643.

XX Novel human amine receptor polypeptide useful as research agents and

PT materials for discovery of treatments and diagnostics to human disease

PS Claim 8; Fig 1; 24pp; English.

XX The present sequence represents a human amine receptor. The polypeptide

CC is a G-protein coupled receptor. It was identified as an amine receptor.

CC as a result of amino acid sequence homology to the rat amine receptor.

CC The protein also exhibits homology to a human dopamine D2 receptor.

CC The polynucleotide sequence is used as a source of probes and primers,

CC and for chromosome mapping studies. The polypeptide may be used to

CC identify modulators and ligands.

XX Sequence 337 AA;

SO Query Match 100.0%; Score 1785; DB 23 Length 337;
Best Local Similarity 100.0%; Pred. No. 1.5e-186
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLTIIVGNFVAVAS 60
1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLTIIVGNFVAVAS 60

DB 1 YFKAATPTNFFLLSLALADMFGLVLPSTIRSVESCFEFDLCRLHTYDTECLT 120
61 YFKAATPTNFFLLSLALADMFGLVLPSTIRSVESCFEFDLCRLHTYDTECLT 120

QY 121 SIHFICFISIDRHCALCDPLIPSKFTVVALRIILAGWVPAAVTSLEFXTDVEVERLS 180
121 SIHFICFISIDRHCALCDPLIPSKFTVVALRIILAGWVPAAVTSLEFXTDVEVERLS 180

DB 121 SIHFICFISIDRHCALCDPLIPSKFTVVALRIILAGWVPAAVTSLEFXTDVEVERLS 180
181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240
181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240

QY 181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240
181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240

DB 241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300
241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300

QY 301 NPITVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337
301 NPITVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

DB 301 NPITVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

RESULT 4
ABP56910
ID ABP56910 standard; Protein; 337 AA.

AC ABP56910;

DT 08-APR-2003 (first entry)

XX Human orphan GPCR protein SEQ ID NO:2.

XX Human: orphan G protein-coupled receptor; GPCR; 1NR; schizophrenia;

KW putative neurotransmitter receptor; transgenic mouse.

XX Homo sapiens.

OS WO2003001882-A2.

PN WO2003001882-A2.

PD 09-JAN-2003.

XX 25-JUN-2002; 2002WO-US20269.

PF 26-JUN-2001; 2001US-301281P.

PR 14-DEC-2001; 2001US-340380P.

XX (DELT-) DELTAGEN INC.

PA Allen KD;

PI WPI; 2003-201449/19.

DR

DR N-PSDB; AB222929.

XX Transgenic mice comprising disruptions in a putative neurotransmitter

PT receptor (PNR) gene, useful as models for studying diseases associated

PT with a disruption in a PNR gene, or for identifying agents for treating

PT schizophrenia

XX Disclosure; Fig 2; 60pp; English.

XX The present invention describes a transgenic mouse comprising a

CC disruption in a putative neurotransmitter receptor (PNR) gene, where

CC there is no native expression of endogenous PNR gene. PNR has

CC neuroleptic activity. The transgenic mice are useful as models for

CC studying diseases, disorders or conditions associated with phenotypes

CC relating to a disruption in a PNR gene. The transgenic mice and cells

CC comprising disruptions in PNR genes are also useful in evaluating

CC various treatments or identifying agents for treating disease states

CC in which PNR may be involved, such as schizophrenia. The present

CC sequence represents a human orphan G protein-coupled receptor which is

CC a PNR used in an example from the present invention.

XX Sequence 337 AA;

SO Query Match 100.0%; Score 1785; DB 24; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.5e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLTIIVGNFVAVAS 60
1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLTIIVGNFVAVAS 60

DB 1 MRAVFIOGAEEHPAFCYQVNGSCPRTVHTLGIOLVYLLCAAGMLTIIVGNFVAVAS 60
61 YFKAATPTNFFLLSLALADMFGLVLPSTIRSVESCFEFDLCRLHTYDTECLT 120
61 YFKAATPTNFFLLSLALADMFGLVLPSTIRSVESCFEFDLCRLHTYDTECLT 120

QY 121 SIHFICFISIDRHCALCDPLIPSKFTVVALRIILAGWVPAAVTSLEFXTDVEVERLS 180
121 SIHFICFISIDRHCALCDPLIPSKFTVVALRIILAGWVPAAVTSLEFXTDVEVERLS 180

DB 121 SIHFICFISIDRHCALCDPLIPSKFTVVALRIILAGWVPAAVTSLEFXTDVEVERLS 180
181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240
181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240

QY 181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240
181 QMLEEMPCVSCQLLNKFKGWLNFLEFVPCCLIMISLYKIFVATROAQOITTSKSL 240

DB 241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300
241 AGAAKHERKAKTIGIVGYLLCWLPTIDTWDSLHITPPLVDFDIWFAYFNSAC 300

QY 301 NPITVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337
301 NPITVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

DB 301 NPITVFSYQWFRKALKLTLSQKVFSPQTRVDLYOE 337

RESULT 5
ABB99760
ID ABB99760 standard; Protein; 337 AA.

AC ABB99760;

DT 24-MAR-2003 (first entry)

XX Amino acid sequence of a protein 43% identical to human TA5 receptor.

DE Human; trace amine receptor; TA5 receptor; G protein-coupled receptor;

XX GPCR; chromosome 6; haematological disorder; CNS disorder; asthma;

KW chronic obstructive pulmonary disease; COPD; cardiovascular disorder;

KW gastrointestinal disorder; cancer; diabetes; obesity;

KW genitourinary disorder.

XX Homo sapiens.

OS WO200299107-A2.

PN WO200299107-A2.

PD 12-DEC-2002.

DR

XX 06-JUN-2002; 2002WO-EP06206.
 PF
 XX 07-JUN-2001; 2001US-296136P.
 PR 17-APR-2002; 2002US-372809P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Zhu Z;
 XX
 DR WPI: 2003-140624/13.
 XX N-PSDB; ABZ23221.
 XX
 PT New polynucleotide encoding a G protein-coupled receptor polypeptide
 PT useful for treating diseases, e.g. hematological, cardiovascular,
 PT gastrointestinal or genitourinary disorders, asthma, cancer, diabetes,
 PT obesity -
 XX
 PS Disclosure; Page 153-154; 154pp; English.
 XX
 XX The present sequence represents a protein which is 43% identical to a
 CC human trace amine receptor designated TAS receptor. TAS is a
 CC G protein-coupled receptor (GPCR), located on chromosome 6. TAS
 CC polypeptides and polynucleotides are useful for the preparation of
 CC a medicament for modulating the activity of the GPCR in a disease,
 CC e.g. hematological disorders, a CNS disorder, chronic obstructive
 CC pulmonary disease (COPD), asthma, a cardiovascular disorder, a
 CC gastrointestinal disorder, cancer, diabetes, obesity or genitourinary
 CC disorder.
 CC
 XX Sequence 337 AA;
 SQ
 Query Match 100.0%; Score 1785; DB 24; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.5e-186;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEBHPAFCYQVNGSCPRTVHTLGIQVLYLTCAGMLITVIGNVFAVAVS 60
 DB 1 MRAVFIOGAEBHPAFCYQVNGSCPRTVHTLGIQVLYLTCAGMLITVIGNVFAVAVS 60
 QY 61 YFKALHTPTNFFLLSLALADMFGLVLPLSTIRSVSCWFGDFLCRLHTYDTLFCLT 120
 DB 61 YFKALHTPTNFFLLSLALADMFGLVLPLSTIRSVSCWFGDFLCRLHTYDTLFCLT 120
 QY 121 SIFHLCTISIDRCAICDPLLYPSKFTYKVALRTILAGWGPAAVTSLEFVTVETRLS 180
 DB 121 SIFHLCTISIDRCAICDPLLYPSKFTYKVALRTILAGWGPAAVTSLEFVTVETRLS 180
 QY 121 SIFHLCTISIDRCAICDPLLYPSKFTYKVALRTILAGWGPAAVTSLEFVTVETRLS 180
 DB 121 SIFHLCTISIDRCAICDPLLYPSKFTYKVALRTILAGWGPAAVTSLEFVTVETRLS 180
 QY 181 QMLEEMPCVSGSCQLLNKFMGMNLFPEVPCILMISLYVIFVAVTRQAOITLTKSL 240
 DB 181 QMLEEMPCVSGSCQLLNKFMGMNLFPEVPCILMISLYVIFVAVTRQAOITLTKSL 240
 QY 241 AGAAKHERKAAKTIGIVGTYLLCMLPFTIDTMDVSLHFTTPPLVDIFTFWAFYFNSAC 300
 DB 241 AGAAKHERKAAKTIGIVGTYLLCMLPFTIDTMDVSLHFTTPPLVDIFTFWAFYFNSAC 300
 QY 301 NPITVYSYQWFKRAKLTLSQKFSQTRVVDIKQE 337
 DB 301 NPITVYSYQWFKRAKLTLSQKFSQTRVVDIKQE 337
 QY 301 NPITVYSYQWFKRAKLTLSQKFSQTRVVDIKQE 337
 DB 301 NPITVYSYQWFKRAKLTLSQKFSQTRVVDIKQE 337

RESULT 6
 ABP81936
 ID ABP81936 standard; Protein; 337 AA.
 AC ABP81936;
 XX
 XX 04-MAR-2003 (first entry)
 DE Human putative neurotransmitter receptor protein SEQ ID NO:358.
 XX
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 XX WO200261087-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 19-DEC-2001; 2001WO-US50107.
 XX
 XX 19-DEC-2000; 2000US-257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 XX Burnier GC, Roush CL, Brown JP;
 XX
 XX WPI: 2003-045718/04.
 XX
 XX N-PSDB; ABZ42784.
 XX
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX
 XX Disclosure; Fig 1; 523pp; English.
 PS
 XX
 XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnoses. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.
 CC
 XX Sequence 337 AA;
 SQ
 Query Match 100.0%; Score 1785; DB 24; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.5e-186;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRAVFIOGAEBHPAFCYQVNGSCPRTVHTLGIQVLYLTCAGMLITVIGNVFAVAVS 60
 DB 1 MRAVFIOGAEBHPAFCYQVNGSCPRTVHTLGIQVLYLTCAGMLITVIGNVFAVAVS 60
 QY 61 YFKALHTPTNFFLLSLALADMFGLVLPLSTIRSVSCWFGDFLCRLHTYDTLFCLT 120
 DB 61 YFKALHTPTNFFLLSLALADMFGLVLPLSTIRSVSCWFGDFLCRLHTYDTLFCLT 120

QY 121 SFHLCFISIDRHCAICDPLLYPSKFTVVALRYILAGNCVPAAYTSLFYDVTETRLS 180
 DB 121 SFHLCFISIDRHCAICDPLLYPSKFTVVALRYILAGNCVPAAYTSLFYDVTETRLS 180
 QY 181 QMLEEMPCVSCOLLNKFWMGLNPFLEFVPCCLIMISLVKIFVATRQAQITTLTSL 240
 DB 181 QMLEEMPCVSCOLLNKFWMGLNPFLEFVPCCLIMISLVKIFVATRQAQITTLTSL 240
 QY 241 AGAAKHERKAATLGIIVGIVYLLCWLPTIDTMDVDSLHFIIPPLVFDFIFMFAVNSAC 300
 DB 241 AGAAKHERKAATLGIIVGIVYLLCWLPTIDTMDVDSLHFIIPPLVFDFIFMFAVNSAC 300
 QY 301 NPITYVSYQWFRKALKLTLSQKVFSPQRTTYDLYOE 337
 DB 301 NPITYVSYQWFRKALKLTLSQKVFSPQRTTYDLYOE 337

RESULT 7
 AAG65596
 ID AAG65596 standard; Protein; 321 AA.
 AC AAG65596;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE Human putative neurotransmitter receptor.
 XX
 KM G-protein coupled receptor; GPCR; human; therapeutic; gene therapy;
 KW neurotransmitter receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200172839-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US09524.
 XX
 PR 27-MAR-2000; 2000US-192326P.
 PR 15-AUG-2000; 2000US-0637603.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Wang A, Cravchik A, Di Francesco V, Beasley EM;
 DR WPI; 2001-611615/70.
 XX
 PT New human G-protein coupled receptor, useful for identifying specific
 PT modulators, potential therapeutic agents, is related to the
 PS neurotransmitter receptor family -
 XX
 PS Disclosure: Fig 2; 63pp; English.

The invention provides a human G-protein coupled receptor (GPCR). The GPCR is useful as target for identifying specific modulators and binding agents, potentially useful as human therapeutic agents, and especially for control of diseases in which GPCR is implicated, and for production of specific antibodies (Ab), or to elicit other immune responses. GPCR may be used as reagents for determination of the level of GPCR or its binding partners, as tissue marker, as therapeutics and for pharmacogenomic studies. Ab are useful for isolation and purification of GPCR, and for determination of GPCR, in diagnosis and monitoring. Ab can be used in pharmacogenomic analysis, for tissue typing, and as therapeutic modulators of GPCR. GPCR nucleic acids are useful for recombinant expression of the protein, and as source of primers and probes (for diagnosis) and of antisense sequences and ribozymes (for therapy). They can be used for identifying modulators of its expression, monitoring gene expression during therapy, identifying mutations in the GPCR-encoding gene, construction of gene therapy vectors and preparing transgenic animals, used to study function of GPCR and to identify modulators. The present sequence represents a human putative neurotransmitter receptor.

XX SQ Sequence 321 AA:
 Query Match 95.4%; Score 1703; DB 22; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e-177;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CYOVNCSCEPTVHTLGIQVLYLTCAAGMLIYLGWVFVAFVSYFKALHTPPNLLST 76
 DB 1 CYOVNCSCEPTVHTLGIQVLYLTCAAGMLIYLGWVFVAFVSYFKALHTPPNLLST 60
 QY 77 ALADNGLGLVLPSTIRSVSCWFGDFLCRLHTLIDLPCLTSIFHLCFISIDRHCAI 136
 DB 61 ALADNGLGLVLPSTIRSVSCWFGDFLCRLHTLIDLPCLTSIFHLCFISIDRHCAI 120
 QY 137 CDPLLYPSKFTVVALRYILAGNCVPAAYTSLFYDVTETRLSOMLEEMPCVSCOLL 196
 DB 121 CDPLLYPSKFTVVALRYILAGNCVPAAYTSLFYDVTETRLSOMLEEMPCVSCOLL 180
 QY 197 NKFWMGLNPFLEFVPCCLIMISLVKIFVATRQAQITTLTSLAGAAKHERKAATLGI 256
 DB 181 NKFWMGLNPFLEFVPCCLIMISLVKIFVATRQAQITTLTSLAGAAKHERKAATLGI 240
 QY 257 VVGIVYLLCWLPTIDTMDVDSLHFIIPPLVFDFIFMFAVNSACNPITYVSYQWFRKAL 316
 DB 241 VVGIVYLLCWLPTIDTMDVDSLHFIIPPLVFDFIFMFAVNSACNPITYVSYQWFRKAL 300
 QY 317 KLTLSQKVFSPQRTTYDLYOE 337
 DB 301 KLTLSQKVFSPQRTTYDLYOE 321

RESULT 8
 ABJ37891
 ID ABJ37891 standard; Protein; 339 AA.
 AC ABJ37891;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE NOVX protein sequence SEQ ID NO 28.

XX KM Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
 KM vulnerable; virucide; antibacterial; protozoacide; fungicide; nootropic;
 KM antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
 KM anticonvulsant; antidiabetic; analgesic; dermatological; keratolytic;
 KM antiseborrheic; antirheumatic; antiarthritic; antiinflammatory; anti-HIV;
 KM cytostatic; antitumoric; antipsoriatic; hypotensive; osteopathic;
 KM antidiabetic; antidiabetic; antiallergic; haemostatic;
 KM neuroleptic; antidepressant; antinfertility; NOVX; human disease;
 KM NOVA-associated disorder; trauma; viral; bacterial; fungal; protozoal;
 KM parasitic infection; Alzheimer's disease; stroke; forensic biology;
 KM immunogen; non-human transgenic animal; gene therapy.

XX OS Unidentified.
 XX
 PN WO200281517-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 22-JAN-2002; 2002WO-US02064.
 XX
 PR 19-JAN-2001; 2001US-262892P.
 PR 23-JAN-2001; 2001US-263598P.
 PR 24-JAN-2001; 2001US-263799P.
 PR 25-JAN-2001; 2001US-264117P.
 PR 25-JAN-2001; 2001US-264139P.
 PR 26-JAN-2001; 2001US-264478P.
 PR 30-JAN-2001; 2001US-263351P.
 PR 02-MAR-2001; 2001US-272870P.
 PR 14-MAR-2001; 2001US-275927P.
 PR 14-MAR-2001; 2001US-275990P.
 PR 15-MAR-2001; 2001US-276449P.

XX (SYNA-) SYNAPTIC PHARM CORP.
 PA Bonini JA, Borowsky BE;
 XX WPI: 2000-610854/58.
 DR N-PSDB: AAA75824.
 XX
 PT New recombinant nucleic acid molecules, with sequences identical to the
 PT human and rat SNORF1 receptor-encoding nucleic acid molecules and
 PT possessing the structural motif characteristics of a G-protein -
 XX
 PS Disclosure: Fig 2A-B; 19pp; English.
 XX
 CC The present sequence represents a SNORF1 receptor. The SNORF1 nucleic
 CC acids may be used as probes to obtain homologous nucleic acids from other
 CC species and to detect the existence of nucleic acids having complementary
 CC sequences in samples. The nucleic acids may also be used to express the
 CC receptors they encode in transfected cells. Also, use of the receptor
 CC encoded by the SNORF1 receptor nucleic acid sequence enables the
 CC discovery of the endogenous ligand and to elucidate the role of the
 CC SNORF1 receptor. The receptor may be employed for designing drugs for
 CC treating various pathological conditions such as chronic and acute
 CC inflammation, arthritis, autoimmune diseases, transplant rejection,
 CC bacterial and fungal infections, AIDS, pain, psychotic and neurological
 CC disorders. Transfected cells with the receptor may be used to test
 CC compounds which bind to the receptor and which activate or inhibit the
 CC functional responses.
 CC
 XX Sequence 348 AA:
 SQ
 Query Match 45.5%; Score 812.5; DB 21; Length 348;
 Best Local Similarity 46.1%; Pred. No. 3.9e-80;
 Matches 152; Conservative 64; Mismatches 105; Indels 9; Gaps 3;
 QY 17 CYO-VNGSCPRTVHTLGVLVYLTCAAGMLIIVGNVAVAVSYFKAHPTNELL 75
 DB 14 CKNVNESCIKTPYSPGRSILYAVLGFCAVLAFCNLMVAILHFKQLHTPTNELL 73
 QY 76 LALDMFGLVLPLSTIRSVESCFEGDFLCRLHTYDLPCLNLSIFHLCTSIDRHA 135
 DB 74 LACADFIVGVTVMPSTVRSVESCWFYFGDSYCFHCFPTSCFASLFLHLCISYDRYA 133
 QY 136 ICDPLLYPSKFTVRAVRLIAGVGPAAVYLSFLTYDVEFRLSOMLEMPVSCQLL 195
 DB 134 VTDPLTYPKFTVSVSGICIVLSWFFSVYSISIFTGANEIEELVALVTCVGGCQAP 193
 QY 196 LKRFWGMNFPLEFVPCIMISLYKIFVATROAOI-TLTSKSLAGA-----AKHE 247
 DB 194 LKQNVVLCFLFLFPNVAWFIYSKIFVAHQAKISTASQOSSSESEKERYAKRE 253
 QY 248 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPIIYF 307
 DB 254 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPIIYF 313
 QY 308 STQWFRKAKLTLSOKVSPQTRIVDLYOE 337
 DB 314 FYQWFGKAIKILIVSGKVLATDSSSTNLESE 343
 RESULT 10
 ID ABB98168 standard; Protein; 348 AA.
 AC ABB98168;
 DT 05-NOV-2002 (first entry)
 XX Human AXOR 106 amino acid sequence.
 DE AXOR 106; GPCR; G-Protein Coupled receptor; antihistaminic; antifungal;
 XX antitumor; antiprotoczoal; anti-HIV; analgesic; cytostatic; antidiabetic;
 KW anorectic; anabolic; antilastmatic; antiparkinsonian; cardiast;

KW hypertensive; hypotensive; diuretic; osteopathic; antianginal;
 KW cerebroprotective; antitumor; antiallergic; human; bacterial; fungal;
 KW protozoan; viral; infection; human immunodeficiency virus; HIV-1;
 KW HIV-2; pain; cancers; diabetes; obesity; anorexia; bulimia; asthma;
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;
 KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 KW stroke; ulcer; allergy; vaccine; screening; GPR57.
 XX
 OS Homo sapiens.
 XX GB2372249-A.
 PN 21-AUG-2002.
 PD 18-OCT-2001; 2001GB-0025067.
 PF 20-OCT-2000; 2000US-242399P.
 PR (SMK) SMITHKLINE BEECHAM CORP.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 XX Shabon U, Elshourbagy N, Agarwal P, Quillen JW, Gattu M;
 PI WPI: 2002-610876/66.
 DR N-PSDB: ABQ79377.
 DR
 XX New G-protein coupled receptor protein, useful for developing
 PT diagnostic reagents and for treating viral infections, pain, cancers,
 PT diabetes, and development of vaccines -
 PT
 XX Claim 1 (c): Page 30; 37pp; English.
 PS
 XX The invention relates to a polypeptide designated AXOR, which is a member
 CC of the G-protein coupled 7 trans-membrane receptor family. The activity
 CC of the polypeptide of the invention may be described as, antibacterial,
 CC antifungal, antiviral, antiprotoczoal, anti-HIV, analgesic, cytostatic,
 CC antidiabetic, anorectic, anabolic, antilastmatic, antiparkinsonian,
 CC cardiant, hypertensive, hypotensive, diuretic, osteopathic, antianginal,
 CC cerebroprotective, antitumor and antiallergic. Polynucleotides of the
 CC invention can be used to treat diseases including bacterial, fungal,
 CC protozoan and viral infections, human immunodeficiency virus, (HIV-1,
 CC HIV-2), pain, cancers, diabetes, obesity, anorexia, bulimia, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 CC stroke, ulcers, and allergies. Polypeptides and polynucleotide may also
 CC be used in vaccines. The polypeptide may be used in low capacity
 CC screening methods and also in high-throughput screening formats. The
 CC current sequence represents the AXOR 106 amino acid sequence.
 CC
 XX Sequence 348 AA:
 SQ
 Query Match 45.5%; Score 812.5; DB 23; Length 348;
 Best Local Similarity 46.1%; Pred. No. 3.9e-80;
 Matches 152; Conservative 64; Mismatches 105; Indels 9; Gaps 3;
 QY 17 CYO-VNGSCPRTVHTLGVLVYLTCAAGMLIIVGNVAVAVSYFKAHPTNELL 75
 DB 14 CKNVNESCIKTPYSPGRSILYAVLGFCAVLAFCNLMVAILHFKQLHTPTNELL 73
 QY 76 LALDMFGLVLPLSTIRSVESCFEGDFLCRLHTYDLPCLNLSIFHLCTSIDRHA 135
 DB 74 LACADFIVGVTVMPSTVRSVESCWFYFGDSYCFHCFPTSCFASLFLHLCISYDRYA 133
 QY 136 ICDPLLYPSKFTVRAVRLIAGVGPAAVYLSFLTYDVEFRLSOMLEMPVSCQLL 195
 DB 134 VTDPLTYPKFTVSVSGICIVLSWFFSVYSISIFTGANEIEELVALVTCVGGCQAP 193
 QY 196 LKRFWGMNFPLEFVPCIMISLYKIFVATROAOI-TLTSKSLAGA-----AKHE 247
 DB 194 LKQNVVLCFLFLFPNVAWFIYSKIFVAHQAKISTASQOSSSESEKERYAKRE 253
 QY 248 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPIIYF 307
 DB 254 RKAATLGIIVGIVLCLMFLPTIDPMVDSLHFTTPPLVFIJFIWFAYNSACNPIIYF 313
 QY 308 STQWFRKAKLTLSOKVSPQTRIVDLYOE 337
 DB 314 FYQWFGKAIKILIVSGKVLATDSSSTNLESE 343

PF 06-APR-1999; 9905-0286805.
 XX
 PR 06-APR-1999; 9905-0286805.
 XX
 PA (SYNA-) SYNAPTRIC PHARM CORP.
 XX
 PI Bonini JA, Borowsky BE;
 XX
 DR WPI; 2000-610854/58.
 N-PSDB; AAA75825.
 XX
 PT New recombinant nucleic acid molecules, with sequences identical to the
 XX human and rat SNORF1 receptor-encoding nucleic acid molecules and
 XX possessing the structural motif characteristics of a G-protein
 XX
 PS Disclosure; Fig 4A-B; 19pp; English.
 XX
 CC The present sequence represents a SNORF1 receptor. The SNORF1 nucleic
 CC acids may be used as probes to obtain homologous nucleic acids from other
 CC species and to detect the existence of nucleic acids having complementary
 CC sequences in samples. The nucleic acids may also be used to express the
 CC receptors they encode in transfected cells. Also, use of the receptor
 CC encoded by the SNORF1 receptor nucleic acid sequence enables the
 CC discovery of the endogenous ligand and to elucidate the role of the
 CC SNORF1 receptor. The receptor may be employed for: designing drugs for
 CC treating various pathophysiological conditions such as chronic and acute
 CC inflammation, arthritis, autoimmune diseases, transplant rejection,
 CC bacterial and fungal infections, AIDS, pain, psychotic and neurological
 CC disorders. Transfected cells with the receptor may be used to test
 CC compounds which bind to the receptor and which activate or inhibit the
 CC functional responses.
 CC
 XX
 SQ Sequence 338 AA;
 XX
 Query Match 44.6%; Score 795.5; DB 21; Length 338;
 Best Local Similarity 45.5%; Pred. No. 2.7e-78;
 Matches 150; Conservative 64; Mismatches 107; Indels 9; Gaps 3;
 XX
 QY 17 CYQ-VNGSCPRTVHTGLDLYLYLTCAGMLIVLGNVAFAPAVSYKALHTPTNLLLS 75
 DB 4 CRENVGSCIKSSYSWPRALIXAVLGALLAVFENLLVITAILHFKQLHTFTNPLVAS 63
 QY 76 LALADFLGLVLPSTIRSVESCFPGFLCRHLYLDI LFCULSIFHLCTSIDRCA 135
 DB 64 LACADFLVGVTVAPFSTVRSVEGCMYFCPTCYCFHRCFPI SFCFASLFLHCCISIDRYVA 123
 QY 136 ICDDPLLYPSKFFRVNLRITLAGMGVPAAYTSLFLTDV ERTLSQLMELRMPVGSQOLL 195
 DB 124 VTDPLTYPTKFTISVSGVCIASWFSVTYSIFYTGA EBGIEELVVALTCVGCQAP 183
 QY 196 LKFMGMNFPLEFVPCILIMISLYKIFVAVTRAOQIT TSKSLAGA-----AKHE 247
 DB 184 LKQNVAVLCFLFLFPLTVVAVFLYGRILFLVAKQAKIK SAMQPASSSYKERVARE 243
 QY 248 KRAAKTLGVVGIYLLCMLPFTIDWVDSLHFTTTPPLV DITMFAYENSACNPITTYF 307
 DB 244 KRAAKTLGIAMAFVLSMLPYIIDAVIDAYMNFITPAVY EILVMCVYVSANPNITAYF 303
 QY 308 SYOMFRKALKLTLQKVFSPQRTVDLYOE 337
 DB 304 FYWFRKAIKILYSGVFRADSRITLSE 333
 XX
 RESULT 13
 ID AAG80970 standard; protein; 345 AA.
 XX
 AC AAG80970;
 XX
 DT 28-AUG-2001 (first entry)
 XX
 DE Human nGPCR40 #2.
 XX

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000MO-US31581.
 XX
 PR 16-NOV-1999; 9905-0165838.
 XX
 PR 17-NOV-1999; 9905-0166071.
 XX
 PR 19-NOV-1999; 9905-0166678.
 XX
 PR 28-DEC-1999; 9905-0173396.
 XX
 PR 22-FEB-2000; 2000US-0184129.
 XX
 PR 28-FEB-2000; 2000US-0185421.
 XX
 PR 28-FEB-2000; 2000US-0185554.
 XX
 PR 02-MAR-2000; 2000US-0186530.
 XX
 PR 03-MAR-2000; 2000US-0186811.
 XX
 PR 09-MAR-2000; 2000US-0188114.
 XX
 PR 17-MAR-2000; 2000US-0190310.
 XX
 PR 21-MAR-2000; 2000US-0190800.
 XX
 PR 20-APR-2000; 2000US-0198568.
 XX
 PR 02-MAY-2000; 2000US-0201190.
 XX
 PR 08-MAY-2000; 2000US-0203111.
 XX
 PR 25-MAY-2000; 2000US-0207094.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogel G, Wood LS, Parodi LA, Hiesch RR, Land P, Slightom J;
 PI Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
 DR WPI; 2001-389826/41.
 N-PSDB; AAH51010.
 XX
 DR New G protein-coupled receptor (nGPCR-x) and its encoding
 XX polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 XX
 PS Claim 37; Page 91; 26pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
 CC sequence is one such G protein-coupled receptor. GPCRs are also known as
 CC seven transmembrane receptors and function in signal transduction. The
 CC nGPCR coding sequences are useful for screening a human to diagnose a
 CC disorder affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCR are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCR in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCR activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
 CC diseases e.g. inflammatory bowel disease.
 CC
 XX
 SQ Sequence 345 AA;
 XX
 Query Match 44.1%; Score 786.5; DB 22; Length 345;
 Best Local Similarity 44.2%; Pred. No. 2.7e-77;
 XX

Search completed: August 26, 2003, 14:23:51
Job time : 46 secs

```

XX OS Homo sapiens.
XX PN WO200261075-A1.
XX PD 08-AUG-2002.
XX PF 31-JAN-2002; 2002MO-JP00773.
XX PR 01-FEB-2001; 2001JP-0025037.
XX PR 30-MAR-2001; 2001JP-0102559.
XX PR 04-APR-2001; 2001JP-0105435.
XX PA (TAKEDA ) TAKEDA CHEM IND LTD.
XX PI Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;
XX N-PSDB: ABO74527, ABO74530.
XX DR WPI: 2002-608518/65.
XX DR N-PSDB: ABO74527, ABO74530.
XX PT G-protein coupled receptor protein expressed in human kidney for design
XX PT of drugs and reagents for treatment and diagnosis of a broad range of
XX PT diseases including cancer -
XX PS Claim 1, Fig 2; 106pp; Japanese.
XX
CC The present sequence represents a human G protein-coupled receptor
CC protein designated TGR36 (I), which is expressed in human kidney. (I)
CC has nootropic, neuroleptic, vasotropic, hypotensive, antiinflammatory,
CC antidiabetic, immunosuppressive, antiviral, antibacterial, nephrotropic
CC and cytoskeletal activities, and can be used in the modification or
CC inhibition of signal transmission mediated by TG31 and associated with
CC a broad range of disorders. (I) is useful for treatment, prevention and
CC diagnosis of central nervous system diseases (such as Alzheimer's
CC disease, anorexia and dementia), metabolic diseases (such as diabetes
CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian
CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),
CC circulatory diseases (such as hypertension, atherosclerosis and angina),
CC inflammatory diseases (such as allergy and rheumatism), respiratory
CC diseases (such as asthma and bronchitis), digestive diseases (such as
CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune
CC diseases), and infections (such as AIDS, pneumonia and influenza).
XX
SQ Sequence 345 AA:
Query Match 44.1%; Score 786.5; DB 23; Length 345;
Best Local Similarity 44.2%; Pred. No. 2.7e-77;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;
QY 17 CY-QVNGSCPRTVHTLQIQLVYLTCAGMLIVLGNVFAFVAVSYKALHTPTNELL 75
DB 14 CYANVNGSCVKIPFSGSRVILIVFGAVLAVPGNLWMISILHFKQLHSPTNVLAS 73
QY 76 LALADMFLGLVLPSTIRSVESCFEGDFLCRLHTYLDLFLCTISIFHLCTSIDRCA 135
DB 74 LACADFLVGVTFVAFSMVTVESCFEGDFLCRLHTYLDLFLCTISIFHLCTSIDR 133
QY 136 ICDPLLYPSKFTVRAVRLAGMGVPAVYSLFLYDVEVRLSQMLEMPVSGCOLL 195
DB 134 VTDPLVYPTKFTVSVSGICISWILPLMTSGAVFTTYGVDGLELSDALNCTIGGQTV 193
QY 196 LKRFMGMLNPLFEVCLIMISLYKIFVAVTRQAOOI-TTLRSK-----LAGAKHE 247
DB 194 VNQNMVLTDFLSFPIFTIMILYGNIFLVARQAKIEWTSGTSSSESYKARVARE 253
QY 248 RRAAKTLGIVGILLCVLPFTIDMVDSILHFTIPPLVFDITWFATFNSACNPITYF 307
DB 254 RRAAKTLGIVVAFVAFMSLPSIDSLIDAFMGFTIACIYEICCCWCAVYNSANPLIYAL 313
QY 308 SYOMFRKALKLTSOKVFSPTFTVLDYOE 337
DB 314 FYFWFRKALKIVITGOVLKNSATIMLDFSE 343

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:22:32 ; Search time 19 seconds
(without alignments)
1705.729 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785

Sequence: 1 MRAVFIOGAEEHPAFCYOV.....ITLSQ:VTFSPQRTVLYXOE 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_76:***
2: PIR1:***
3: PIR3:***
4: PIR4:***

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	337	2	JCS832
2	446.5	25.0	387	2	S55550
3	446.5	25.0	406	2	S55549
4	420	23.5	359	2	JC4120
5	419	23.5	515	2	A40491
6	418	23.4	517	2	A45121
7	417	23.4	483	2	A25896
8	416.5	23.3	358	2	JQ1278
9	415.5	23.3	359	2	JH0449
10	413.5	23.2	477	2	S71323
11	412.5	23.1	429	2	S65656
12	412.5	23.1	466	2	JN0765
13	412.5	23.1	466	2	I57959
14	412.5	23.1	499	2	S65657
15	411	23.0	465	2	I51661
16	409.5	22.9	466	2	A33375
17	408	22.9	515	2	JC1525
18	407.5	22.8	374	2	I77467
19	404.5	22.7	436	2	JN0591
20	404.5	22.7	466	2	S36794
21	404	22.6	377	2	B30341
22	401.5	22.5	437	2	I57942
23	400	22.4	464	2	S12591
24	398.5	22.3	359	2	A35008
25	398.5	22.3	363	2	I50475
26	397.5	22.3	459	2	A56849
27	397	22.2	440	2	JC5520
28	396.5	22.2	377	2	A53279
29	394.5	22.1	428	2	A55044

30	393.5	22.0	446	1	DYH0D1	dopamine receptor
31	393	22.0	377	2	S68423	serotonin receptor
32	393	22.0	457	2	I51660	dopamine D1B recep
33	392.5	22.0	444	2	C55886	dopamine receptor
34	392	22.0	451	2	I51859	dopamine D1A recep
35	391.5	21.9	463	2	B56849	dopamine receptor-
36	390.5	21.9	418	2	S00260	beta-2-adrenergic
37	390	21.8	477	1	ORH0B1	beta-1-adrenergic
38	388	21.7	476	2	JC5042	G protein-coupled
39	387.5	21.7	446	2	I47217	dopamine receptor
40	387	21.7	450	2	A55886	dopamine receptor
41	387	21.7	450	2	A38316	alpha-2-adrenergic
42	386.5	21.7	389	2	S68422	serotonin receptor
43	386	21.6	390	2	JN0268	serotonin receptor
44	385.5	21.6	390	2	S58126	serotonin receptor
45	385.5	21.6	418	2	S10855	beta-2-adrenergic

ALIGNMENTS

RESULT 1

JCS832 neurotransmitter receptor - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999

C:Accession: JCS832

R:Zeng, Z.; Fan, P.; Rand, E.; Kyaw, H.; Su, K.; Madlike, V.; Carter, K.C.; Li, Y.

Biochem. Biophys. Res. Commun. 242, 575-578, 1998

A:Title: Cloning of a putative human neurotransmitter receptor expressed in skeletal

A:Reference number: JCS832; PMID:98125534; PMID:9464258

A:Accession: JCS832

A:Molecule type: mRNA

A:Residues: 1-337 <REN>

A:Cross-references: GB:AF021818; NID:g2465431; PIDN:AAC39581.1; PID:g2465432

A:Experimental source: brain

C:Genetics:

A:Map position: 6q23

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; receptor; transmembrane protein

F:29-63/Domain: transmembrane #status predicted <TM1>

F:69-95/Domain: transmembrane #status predicted <TM2>

F:114-118/Domain: transmembrane #status predicted <TM3>

F:149-173/Domain: transmembrane #status predicted <TM4>

F:186-200/Domain: transmembrane #status predicted <TM5>

F:204-229/Domain: transmembrane #status predicted <TM6>

F:253-310/Domain: transmembrane #status predicted <TM7>

F:21/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1785; DB 2; Length 337;

Best local Similarity 100.0%; Pred. No. 4,6e-143; Mismatches 0; Indels 0; Gaps 0;

Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRAVFIOGAEEHPAFCYOVNSCPRTVHTLGIVLYITCAAGMLIIVGNVFAVVS	60
DB	1	MRAVFIOGAEEHPAFCYOVNSCPRTVHTLGIVLYITCAAGMLIIVGNVFAVVS	60
QY	61	YFRALHTPNNFLSLALDMFLGLVLPSTRSVSCWFGDFLCRLHTYIDTLFCLT	120
DB	61	YFRALHTPNNFLSLALDMFLGLVLPSTRSVSCWFGDFLCRLHTYIDTLFCLT	120
QY	121	SIFHLCFISIDRHCACDPLLYPSKFTVVALRYILAGGVPAAYSLFLYDVVETRSL	180
DB	121	SIFHLCFISIDRHCACDPLLYPSKFTVVALRYILAGGVPAAYSLFLYDVVETRSL	180
QY	181	QMLEEMPVCGSCOLLNKGWMLNPLFFVPCILIMISLYVKIFVATROAQDITLTKSL	240
DB	181	QMLEEMPVCGSCOLLNKGWMLNPLFFVPCILIMISLYVKIFVATROAQDITLTKSL	240
QY	241	AGAAKHERAKAATIGIVGIVYLLCMLPFTIDMVNSLHPTIPVDFDIFPAVFNASC	300
DB	241	AGAAKHERAKAATIGIVGIVYLLCMLPFTIDMVNSLHPTIPVDFDIFPAVFNASC	300

OY 301 NPITVSVQWFRKALKTLSQKVSFQRTVDLYQE 337
 |||||
 DB 301 NPITVSVQWFRKALKTLSQKVSFQRTVDLYQE 337

RESULT 2

555550
 5-HT4S receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 26-Aug-1999

C:Accession: S55550

R:Gerald, C.; Adham, N.; Kao, H.T.; Olsen, M.A.; Laz, T.M.; Schechter, L.E.; Bard, J.A.;

EMBO J. 14, 2806-2815, 1995

A:Title: The 5-HT(4) receptor: molecular cloning and pharmacological characterization of

A:Reference number: S55549; MUID:95317299; PMID:7796807

A:Accession: S55550

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-387 <GER>

A:Cross-references: GB:020906; NID:924638; PIDN:AAC52232.1; PID:9244639

C:Superfamily: vertebrate rhodopsin

Query Match 25.0%; Score 446.5; DB 2; Length 387;
 Best Local Similarity 33.1%, Pred. No. 3.5e-30;

Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

OY 33 IQLVYLT-CAAGMLIYLVGNVFAVAFVSKALH-TPNFLLSLALADMFGLVLP 90

DB 17 VEKVVLTFFAMVIMAILGNLWVAVCRDRLKIKTNFYISLAFADLVSVLNAF 76

OY 91 STIRSVSCWFFGDFLCRLHTYLDTLCLTSIFHLCSIDRHCAT-CDPLLYSKFT-V 148

DB 77 GAIELVODIMFEGMFLVRLTSIDVLTASIFHLCCISIDRYAICQPLVYRNKMTPL 136

OY 149 RVALRYILAG-WGVPAAVTSIFL-----YTDVETR-----LSQMLEMPCVG 190

DB 137 RIAL--MLGCGVITPMFISFLPIMGWNNIGIVDIEKRKNHNSSTFCVFNKRPYAI 194

OY 191 SCQILLNKFWGMLNPLFEPVCLIMISLYKIFVATROAQOITTLKSLAGAKHER-- 248

DB 195 TCSVV-----AFYIPFLMLVLAHYRIYTAKEHAQIQMLQR--AGATSESRPQ 241

OY 249 -----KAATLGIVGIYLLCWLPTIDTMVDSLHFTTPPLVDFITMFA 294

DB 242 TADQSHTRMTEETKAKATLCVINGCFCECAFPFVNIYDPFDIVPERKWTAFIMLG 301

OY 295 YFNSACNPITVSVQWFRKALKTLL 320

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

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OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

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OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

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DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

A:Molecule type: mRNA
 A:Residues: 95-259 <DILL>
 A:Cross-references: EMBL:Z48153; NID:984171; PIDN:CAA88170.1; PID:984172
 A:Experimental source: tissue brain
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: neurotransmitter receptor

Query Match 25.0%; Score 446.5; DB 2; Length 406;
 Best Local Similarity 33.1%, Pred. No. 3.6e-30;

Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

OY 33 IQLVYLT-CAAGMLIYLVGNVFAVAFVSKALH-TPNFLLSLALADMFGLVLP 90

DB 17 VEKVVLTFFAMVIMAILGNLWVAVCRDRLKIKTNFYISLAFADLVSVLNAF 76

OY 91 STIRSVSCWFFGDFLCRLHTYLDTLCLTSIFHLCSIDRHCAT-CDPLLYSKFT-V 148

DB 77 GAIELVODIMFEGMFLVRLTSIDVLTASIFHLCCISIDRYAICQPLVYRNKMTPL 136

OY 149 RVALRYILAG-WGVPAAVTSIFL-----YTDVETR-----LSQMLEMPCVG 190

DB 137 RIAL--MLGCGVITPMFISFLPIMGWNNIGIVDIEKRKNHNSSTFCVFNKRPYAI 194

OY 191 SCQILLNKFWGMLNPLFEPVCLIMISLYKIFVATROAQOITTLKSLAGAKHER-- 248

DB 195 TCSVV-----AFYIPFLMLVLAHYRIYTAKEHAQIQMLQR--AGATSESRPQ 241

OY 249 -----KAATLGIVGIYLLCWLPTIDTMVDSLHFTTPPLVDFITMFA 294

DB 242 TADQSHTRMTEETKAKATLCVINGCFCECAFPFVNIYDPFDIVPERKWTAFIMLG 301

OY 295 YFNSACNPITVSVQWFRKALKTLL 320

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

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DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

OY 302 YINGSLNPFILAFINKSFRRAFLITL 327

DB 302 YINGSLNPFILAFINKSFRRAFLITL 327

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Db      60 LAATDILLGLVLPFSALITQLSCKWSKVFNCNITSLVWMLCTASLNTLPMISLDYCA 119
      136 ICDPLLYPSKFT-VRAVRLIAGMGVPAATSLFVTLVETRLSOMLEEMPCVGSOL 194
      120 VDPPLKPVLTARVAISLVPF-WYI--STLSFLSIIGWMSRNETSDNDTIYACKV 176
      195 LNRKFGWMLN-FPLFFVPCLLIMISLYKIFVATROAQITTLTSKSLAGAAKHEKRAKT 253
      177 QVNEVYGLVDGLVTFVLPILIMCITVFRIKIAREQARINHG-SKKAATIREKATV 235
      254 LGIVGGLYLLCMLP-FII-----DTMDSLHHTFPLVNDIFVWFVFNACNPII 304
      236 LAAVMGAFIICWPFYFVYRGLKGDADVAENEVE-----DVLMLGYANSALNPIL 287
      305 YVFSYQWFKKA 315
      288 YALNDRDFRKA 298

```

RESULT 5

A:Accession: A40491
 A:Title: alpha-1-adrenergic receptor - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C:Accession: A40491
 R:Cotechia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988
 A:Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic
 A:Reference number: A40491; MUID:89017157; PMID:2845338
 A:Accession: A40491
 A:Molecule type: mRNA
 A:Residues: 1-515 <COT>
 A:Cross-references: GB:J04084; NID:9619407; PID:AA51964.1; PID:9619408
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 23.5%; Score 419; DB 2; Length 515;
 Best Local Similarity 31.3%; Pred. No. 9.5e-28;
 Matches 110; Conservative 54; Mismatches 135; Indels 52; Gaps 8;

```

      21 NSGCPRTVHTLGIQVLYLTCAGMLITVGNFVAFAVYFKALHPTNFIISLALAD 80
      34 NSTLPQDITRAIS--VGLVGAFLIFAIIGNILVILSV:CNRLRTPPTVFIYNLAD 91
      81 MFTGLVLPSTIRSVSCWPFQDFLCRLHTYLDLTLCL:SIHLCFISIDRHCAIDPL 140
      92 LLSTFVLPFSALLEVIGVWLGRIKFDIWAADVLCCT:SIISLCAISIDRIGVKSL 151
      141 LYSKFTVRAALRYIAGMGVPAATSLFYTVDVETRL:QMLEMPCVG-SCQLLNKF 199
      152 QYPLTVRRKAILALLSVW-----VLSTVISIPLIGMKRPANDKECVTEPEF 202
      200 WG-WLNFPLFFVPCLLIMISLYKIFVATROAQI----- 233
      203 YALFSSIGSPYIPLAVILVMYCRVYIAKRTKMLEAGVAKEMNSKELTLRIHSKNFHE 262
      234 TLTLSKSLAG-----AAK-----HERKAKTGIYVGIYLCWLPPTIDTWDSLHF 280
      263 DTLSSTAKGHNPRSSIAVLLFKFSREKKAATIGIYVGG:FIICWLPFFIATLPGLSLEST 322
      281 ITTP-LVDFIFIMFAVFNACNPIIYVFSYQWFKKALKTLISOKVFSPOTR 330
      323 LKPPDAVFKVYFMVGLGYFNSCNLPITVPCSSKEFRARMLIGCGCRGRRR 373

```

RESULT 6

A:Accession: A45121
 A:Title: alpha-1B adrenergic receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
 C:Accession: A45121; JG2332
 R:Ramalho, C.S.; Denker, J.M.; Perez, D.M.; Galvin, R.J.; Riek, R.P.; Graham, R.M.

J. Biol. Chem. 267, 21936-21945, 1992
 A:Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor
 A:Reference number: A45121; MUID:93016158; PMID:1328250
 A:Accession: A45121
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-517 <RAM>
 A:Cross-references: GB:M99590; NID:q178211
 A>Note: sequence extracted from NCBI backbone (NCBI:P116785)
 A>Note: this translation is not annotated in Genbank entry HUMADREN, release 113.0 #
 R:Wennerg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.
 Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
 A:Title: Cloning, expression and characterization of human alpha adrenergic receptors
 A:Reference number: JG2331; MUID:94296402; PMID:8024574
 A:Accession: JG2332
 A:Molecule type: mRNA
 A:Residues: 1-158, 'P', 160-244, 'H', 246-314, 'F', 316-380, 382-517 <HEI>
 C:Genetics:
 A:Gene: GDB:ADRA1B
 A:Cross-references: GDB:127901; OMIM:104220
 A:Map position: 5q31.1-5q33.2
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:39-72/Domain: transmembrane #status predicted <TM1>
 F:81-111/Domain: transmembrane #status predicted <TM2>
 F:121-146/Domain: transmembrane #status predicted <TM3>
 F:157-184/Domain: transmembrane #status predicted <TM4>
 F:203-227/Domain: transmembrane #status predicted <TM5>
 F:280-320/Domain: transmembrane #status predicted <TM6>
 F:326-360/Domain: transmembrane #status predicted <TM7>

Query Match 23.4%; Score 418; DB 2; Length 517;
 Best Local Similarity 31.8%; Pred. No. 1.2e-27;
 Matches 107; Conservative 52; Mismatches 125; Indels 52; Gaps 8;

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      21 NSGCPRTVHTLGIQVLYLTCAGMLITVGNFVAFAVYFKALHPTNFIISLALAD 80
      34 NSTLPQDITRAIS--VGLVGAFLIFAIIGNILVILSV:CNRLRTPPTVFIYNLAD 91
      81 MFTGLVLPSTIRSVSCWPFQDFLCRLHTYLDLTLCL:SIHLCFISIDRHCAIDPL 140
      92 LLSTFVLPFSALLEVIGVWLGRIKFDIWAADVLCCT:SIISLCAISIDRIGVKSL 151
      141 LYSKFTVRAALRYIAGMGVPAATSLFYTVDVETRLSOMLEEMPCVG-SCQLLNKF 199
      152 QYPLTVRRKAILALLSVW-----VLSTVISIPLIGMKRPANDKECVTEPEF 202
      200 WG-WLNFPLFFVPCLLIMISLYKIFVATROAQI----- 233
      203 YALFSSIGSPYIPLAVILVMYCRVYIAKRTKMLEAGVAKEMNSKELTLRIHSKNFHE 262
      234 TLTLSKSLAG-----AAK-----HERKAKTGIYVGIYLCWLPPTIDTWDSLHF 280
      263 DTLSSTAKGHNPRSSIAVLLFKFSREKKAATIGIYVGG:FIICWLPFFIATLPGLSLEST 322
      281 ITTP-LVDFIFIMFAVFNACNPIIYVFSYQWFKKA 315
      323 LKPPDAVFKVYFMVGLGYFNSCNLPITVPCSSKEFRARA 358

```

RESULT 7

A:Accession: A25896
 A:Title: beta-adrenergic receptor - turkey
 C:Species: Meleagris gallopavo (common turkey)
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 13-Aug-1999
 C:Accession: A25896
 R:Yarden, Y.; Rodriguez, H.; Wong, S.K.F.; Brandt, D.R.; May, D.C.; Bunniar, J.; Hark
 Proc. Natl. Acad. Sci. U.S.A. 83, 6795-6799, 1986
 A:Title: The avian beta-adrenergic receptor: primary structure and membrane topology.
 A:Reference number: A25896; MUID:86313664; PMID:3018746
 A:Accession: A25896
 A:Molecule type: mRNA
 A:Residues: 1-483 <YAR>

A:Molecule type: mRNA
A:Residues: 424-499 <HIR>
A:Cross-references: EMBL:D32202
C:Genetics:
A:Gene: GDB:ADRA1C; ADRA11.1
A:Cross-references: GDB:128088; OMIM:104221
A:Map position: 8p21-8p11.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 23.1%; Score 412.5; DB 2; Length 499;
Best local similarity 32.7%; Pred. No. 3.2e-27;
Matches 112; Conservative 51; Mismatches 126; Indels 53; Gaps 10;

QY 21 NSCPTVHTLGIVLYLTCAGMLII-VLGNVFAVNSYKALHTPTNLLSLAL 78
DB 11 SSMCTOPAPVNSKAILLGVILGGLFCVGLNIIYILSVACHRLHSTHYIYNLAV 70
QY 79 ADMFLGLVLPSTISVSCWFFGDFLCRLHTYLDLTF-LTISIFHLCTISDRHCAICD 138
DB 71 ADLLLTSTVLPFSAIFEVLYGMVAFRCNMAADVLC-TASIMGICITISIDRYIGVSY 130
QY 139 PLTPSKETVYVRLRTILAGMGVPAVTSLELYDYVET-ILSQMLEMPCVGS-CQLLN 197
DB 131 PLTPPTIVTORGLMALCYW-----ALSLVIST-G?LFGMRPAPDEFTICQ--IN 179
QY 198 KFWGWLNFPL---FVPPCLIMISLVYKIEVATRO-----AQGITTL----- 236
DB 180 EEPGYLFSALGSFYLPALITLVMYCVYVAKRESGL(SGLKTDKSDSEQYTLRIHRK 239
QY 237 -----SKSLAGAA-----KHKRAKTIGIV;IYLLCWLPTITDMVDSLH 279
DB 240 NMPAGSGSMASAKTKTHFSYRLKFSREKRAKTIGIV;CFVLCWLPFLVMPIGSFFP 299
QY 280 FTRP-PLVPDIFIFWFAVNSACNPIIYVSYQWFRKALK-TL 320
DB 300 DEKPSFTVRIYVWLGILNSCINPIIYPCSSQEFKRAFO;IVL 341

RESULT 15

151661
dopamine D1C receptor - African clawed frog (fragment.
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #txl_change 13-Aug-1999
C/Accession: I51661
R:Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Nizn, K.; H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A>Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; M0ID:95024150; PMID:7937919
A:Accession: I51661
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-465 <SUG>
A:Cross-references: EMBL:U07865; NID:9559763; PIDN:AA:50830.1; PID:9559764
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 23.0%; Score 411; DB 2; Length 465;
Best local similarity 32.3%; Pred. No. 4.1e-27;
Matches 106; Conservative 56; Mismatches 118; Indels 48; Gaps 11;

QY 31 LGIQLVYLTCAAGMLIIVLGNVFAVNSYKALHTP-TNPLLSLALADMFLGLVLP 89
DB 25 LSLRALTLGLLSTLLSTLGLNVLCAVAKFRHLRSKVTNFEVLSLAVSDLFALLVMP 84
QY 90 LSTIRVSCWFFGDFLCRLHTYLDLTF-LTISIFHLCTISDRHCAICDPLTPSKFTVR 149
DB 85 WKAVTEVAGWVGGDF-CDTWAFDIDMCSTASILNLCITSLDRYWMALASPRYRKWTQR 143
QY 150 VALRTIAGGVPAATSLFLTYDVETRLSQWL-----EEMPCVGS---SCQLLNKFW 200
DB 144 VAFIMIGVAV-----TSLISLIFIPVOLS-WKSHLEALDELNGVNHTEHCDSLNRTY 195

QY 201 GWLNFPL-FVPPCLIMISLVYKIEVATROAQGITTLK-----SLAGA 243
DB 196 AISSSLISFYIPVIMIGTYTRIYAQTQIRRISSLERAVEHAQSCSRLSNSLSKTS 255
QY 244 AKHERRAKTLGIVGVYLLCWLPTITDMVDSLHF-----ITPPLY-----EDIFW 292
DB 256 FRKETVVKTLSTIMGVFVFCWLPFVVLNCMIPFCHMNLPGQNEPBPVCSFTTFNIFW 315
QY 293 FAYNSACNPIIYVSYQWFRKALKTL 320
DB 316 FGWANSLNPIYIAFNAD-FKRAFITL 342

Search completed: August 26, 2003, 14:25:23
Job time : 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2003, 14:21:42 ; Search time 13 Seconds

(without alignments)
1219.077 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785

Sequence: 1 MRAVPIQGAENHPAFCYQV.....LTLSQVPSPTRTVDLYOE 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	459.5	25.7	388	1	5H4_MOUSE P97288 mus musculu
2	455.5	25.5	388	1	5H4_HUMAN O13639 homo sapien
3	452.5	25.4	388	1	5H4_CAVPO 070528 cavia porce
4	446.5	25.0	406	1	5H4_RAT 062758 rattus norv
5	432.5	24.2	466	1	ALIA_MOUSE P97718 mus musculu
6	432.5	24.2	466	1	ALIA_RABIT O02824 oryctolagus
7	422.5	23.7	379	1	5H4_FUGRU P79748 fugu rubrip
8	420	23.5	359	1	HRZR_CAVPO P47747 cavia porce
9	419	23.5	515	1	ALIA_MESAU P18641 mesocricetu
10	418.5	23.4	466	1	ALIA_CAVPO 042574 cavia porce
11	418	23.4	385	1	BIAR_XENLA 09w125 xenopus lae
12	418	23.4	515	1	ALIA_RAT P15823 rattus norv
13	418	23.4	519	1	ALIA_HUMAN P35368 homo sapien
14	417	23.4	483	1	BIAR_MEIGA P07700 meleagris g
15	416.5	23.3	359	1	HRZR_RAT P25102 rattus norv
16	415.5	23.3	359	1	HRZR_HUMAN P25021 homo sapien
17	413.5	23.2	470	1	ALIA_ORYLA 091175 oryzae lat
18	412.5	23.1	466	1	ALIA_HUMAN P43140 homo sapien
19	412.5	23.1	466	1	ALIA_RAT P97922 mus musculu
20	411.5	23.1	358	1	HRZR_MOUSE P42291 xenopus lae
21	411	23.0	465	1	DCOR_XENLA P97717 mus musculu
22	410.5	22.9	514	1	ALIA_MOUSE P18130 bos taurus
23	409.5	22.9	466	1	ALIA_BOVIN P18130 bos taurus
24	407.5	22.8	374	1	SHID_RAT 061285 rattus norv
25	405	22.7	374	1	SHID_MOUSE 061285 rattus norv
26	404.5	22.7	436	1	SH6_RAT P31388 rattus norv
27	404.5	22.7	466	1	BIAR_MOUSE P34771 mus musculu
28	404.5	22.7	467	1	BIAR_BOVIN 09796 bos taurus
29	404	22.6	377	1	SHID_CANFA P18114 canis faml
30	399.5	22.4	467	1	BIAR_SHEEP 028927 ovis aries
31	399.5	22.4	359	1	HRZR_PIG 028998 sus scrofa
32	398.5	22.3	359	1	HRZR_CANFA P17124 canis faml
33	398.5	22.3	363	1	DIDR_CARAU P35406 carassius a

34	397.5	22.3	459	1	DIDR_FUGRU P53452 fugu rubrip
35	397.5	22.3	466	1	BIAR_RAT P18090 rattus norv
36	397	22.2	440	1	SH6_HUMAN P50406 homo sapien
37	396.5	22.2	377	1	SHID_HUMAN P28221 homo sapien
38	395.5	22.2	446	1	DADR_MACMU 077680 macaca mula
39	395.5	22.2	474	1	BIAR_FELCA 097680 felis silve
40	394.5	22.1	428	1	B4AR_MEIGA P79148 canis faml
41	394	22.1	473	1	BIAR_CANFA P79148 canis faml
42	393.5	22.0	446	1	DADR_HUMAN P21728 homo sapien
43	393	22.0	377	1	SHID_RABIT P49145 oryctolagus
44	393	22.0	457	1	DBDR_XENLA P42290 xenopus lae
45	392	22.0	451	1	DADR_XENLA P42289 xenopus lae

ALIGNMENTS

RESULT 1
5H4_MOUSE STANDARD: PRT; 388 AA.
AC P97288; 089003; 089004; 09R2A4;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5-hydroxytryptamine 4 receptor (5-HT-4) (Serootonin receptor) (5-HT4).
GN HTR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Swiss: TISSUE-Brain;
RC MEDLINE-97102706; PubMed-8946946;
RA Claessen S., Sebden M., Journot L., Bockaert J., Dumuis A.;
RT "Cloning, expression and pharmacology of the mouse 5-HT(4l)
RT receptor.";
RL FEBS Lett. 398:19-25(1996).
RN [2]
RP REVISIONS TO C-TERMINUS.
RA Dumuis A.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 5-HT4(A) AND 5-HT4(E)).
RA STRAIN-Swiss: TISSUE-Brain;
RC MEDLINE-99127199; PubMed-9928238;
RA Claessen S., Faye P., Sebden M., Taviaux S., Bockaert J., Dumuis A.;
RT "5-HT4 receptors: Cloning and expression of new splice variants.";
RL Ann. N.Y. Acad. Sci. 861:49-56(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(F)).
RA MEDLINE-9928795; PubMed-10220570;
RC TISSUE-Brain;
RA Claessen S., Sebden M., Becamel C., Bockaert J., Dumuis A.;
RT "Novel brain-specific 5-HT4 receptor splice variants show marked
RT constitutive activity: role of the C-terminal intracellular domain.";
RL Mol. Pharmacol. 55:910-920(1999).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-4:
CC Name-1;
CC IsoId=p97288-1; Sequence=Displayed;
CC Name=5-HT4(A);
CC IsoId=p97288-2; Sequence=VSP_001851;
CC Name=5-HT4(E);
CC IsoId=p97288-3; Sequence=VSP_001852;
CC Name=5-HT4(F);
CC IsoId=p97288-4; Sequence=VSP_001853;

FT	TRANSMEM	138	158		4 (POTENTIAL).
FT	TRANSMEM	193	192		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	159	213		5 (POTENTIAL).
FT	DOMAIN	261	260		CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	214	281		6 (POTENTIAL).
FT	DOMAIN	282	294		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	315		7 (POTENTIAL).
FT	DOMAIN	316	388		CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	7	7		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	DISELTD	93	184		BY SIMILARITY.
FT	LIPID	329	329		PALMITATE (BY SIMILARITY).
FT	VASPLIC	169	169		L -> LERSINGLOGDFHA (in isoform 5-HT4(F)).
FT					/FtId-VSP_001845.
FT	VASPLIC	359	388		RDAEGGOMESQCHPPATSPVLVAQPSDT -> SGCSPVS
FT					SFLLECKNRVPV (in isoform 5-HT4(E)).
FT	VASPLIC	359	388		/FtId-VSP_001846.
FT					RDAEGGOMESQCHPPATSPVLVAQPSDT -> SSGETED
FT	VASPLIC	360	388		RNFNGIRKRLRTPS (in isoform 5-HT4(D)).
FT					/FtId-VSP_001847.
FT	VASPLIC	360	388		DAVEGGOMESQCHPPATSPVLVAQPSDT -> F (in isoform 5-HT4(C)).
FT					/FtId-VSP_001848.
FT	VASPLIC	360	388		HOLEKLPIHPNPELESCEF (in isoform 5-HT4(A)).
FT					DAVEGGOMESQCHPPATSPVLVAQPSDT -> YTVLRGH
FT	VASPLIC	360	388		/FtId-VSP_001850.
FT					Misling (in isoform 5-HT4(G)).
SO	SEQUENCE	388 AA;	43761 MW;	7FCFEC60E7BDF960 CRC64;	
<hr/>					
Oy	Query Match	Best Local Similarity	25.5%;	Score 455.5;	DB 1; Length 388;
	Matches 110;	Conservative	59;	Mismatches 111;	Indels 39; Gaps 1
Oy	33 IQIIVYLT-CAAGMLTIVGNVAVAVSYFAKLH-TPNFFLLSLADAMELGILLVPL	90			
Db	17 VEKVYLTLSTVYLVIAHLISNLVMAVCNDROLRIKIKRYETVLSAEFDLLSVLVMPF	76			
Oy	91 STIRSVESCWFQDFDLCLRTTYLDTEFLCSIFELHSIDBNCAI-CDPLLPERFT-V	14			
Db	77 GAIELVQDDIMVIGSVPCVLVTSIDLVTLLASIFELCISIDRYAIALCOCPILVYRNKMPL	13			
Oy	149 RVALRITLIAG-KGVPAATYSLEL-----YIDVETR-LSOMLEEMPCCVSCOLLINK	19			
Db	137 RIHL-MLGSCWVIPETISFLPTMGOMNNIGIIDLEKKRFQONSNTYCV---FYVRK	19			
Oy	199 FMG-WLNFPLPEFPBCIMLSYKIVIVATROAQDTTSSKLSGAKHER-----	24			
Db	191 PYATICSVAVFIPFLMLVATIRIYTAKEAHHQLOMR--AGASSSRFSQSDQSHST	24			
Oy	249 -----KAKTGIWVGIIQLCMLEPTIDTWVDSLHEITRPLEVDFIEFRAYENSACN	30			
Db	249 HRMRTETRAKAKTCIIMGCRCLAMAPFEVTNIIVDPIDYVGGWTAFMLGTINSGLN	30			
Oy	302 PIIVVESYQWERKAKITL	320			
Db	309 PELYAFLNKSFRRRAFLITL	327			
<hr/>					
RESULT 3					
ID	5H4_CAVPO	STANDARD;	PRT;	388 AA.	
AC	070528;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	5-hydroxytryptamine 4 receptor (5-HT-4) (Superoin receptor) (5-HT4). HTR4.				
OS	Cavia porcellus (Guinea pig).				
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;				
NC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.				
OX	NCBI_TaxID=10141;				

```

[1]
RP SEQUENCE FROM N.A.
RA Van den Wymersert I., Gommeren W., Jurzak M., Verhasselt P., Gordon R.,
RA Leyten J., Luyten W., Bender E.;
RT Cloning and expression of 5-HT4 receptor species and splice
RT variants."
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLYATE
CC CYCLASE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=070528-1; Sequence=Displayed;
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; Y13585; CAA73912.1; .
DR HSSP; P29274; IMMH.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN_RECPT_FL_2; 1.
DR PROSITE; PS00262; G-PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 19
FT TRANSMEM 20 40
FT TRANSMEM 41 58
FT DOMAIN 59 79
FT TRANSMEM 80 93
FT TRANSMEM 94 116
FT DOMAIN 117 137
FT TRANSMEM 138 158
FT DOMAIN 159 192
FT TRANSMEM 193 213
FT DOMAIN 214 260
FT TRANSMEM 261 281
FT DOMAIN 282 294
FT TRANSMEM 295 318
FT DOMAIN 316 388
FT CARBOHD 7 7
FT DISULFD 93 184
FT LPTD 329 329
FT SEQUENCE 368 AA; 43725 MW; 3D45B3A37F6D0D2B CRC64;
SQ
Query Match 25.4%; Score 452.5; DB 1; Length 388;
Best Local Similarity 34.4%; Prcd No. 1,1e-23;
Matches 109; Conservative 61; Mismatches 112; Indels 35; Gaps 11;
OY 33 IQLVYILT-CAAGMLIIVGNVFAVSYFKALH-PTPNELLSIALADNFTGLVLP 90
DB 17 VERVVLLTFELSAVILMLIGNLLVMVAVCRDROLKRIKTYVSLAFADLVSLVMPF 76
OY 91 STISVESCWFQFDFLCRLHYLDLFLCSTIFHLCTSIDRNCRI-CDPLIYPSKFT-V 148
DB 77 GATLEVODIIVYGGEFCLVRTSLDVLTLTASIFHLCCSLDRYVAICOPLYRNKRMPL 136
OY 149 RVALRYTLAG-WGPDVAATYSFL-----YTDVVEIR-LSQWLEMPQVSGCOLINK 198
DB 137 RIAL-MGGGQWVIMFETSLPIMGQANNIGIVDLIERKKNQNSSTYCV---PMVK 190

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OY      199 FMG-WLNEPFEVPCILMISLVKJFEVVAIROAQOITLSSLSLGA-----243
DB      191 PVALTCSVAVFYFIPLLMLATVYRIVYAKKHAARIOVLQAGAPABGRPOPADQSHR 250
OY      244 AKHERRAAKTLGIVGIVLLCNLPETIDMDSLHETPTPLVDFIPMERAVENSACNPT 303
DB      251 MRTEKRAAKTLCLIMCSFCCLCAWAFEVNTIVDPFIDYVVPQGLWTAFMLGIVNSGLNPF 310
OY      304 IYVESYOWPEFKAKLTL 320
DB      311 LVAFLNKSPRRRAFLITL 327

RESULT 4
5H4_RAT STANDARD: PRT; 406 AA.
ID 5H4_RAT
AC Q62758; 089034; Q62757; Q63006;
AD 01-NOV-1997 (Rel. 35, Created)
AD 01-NOV-1997 (Rel. 35, Last sequence update)
AD 28-FEB-2003 (Rel. 41, Last annotation update)
DE 5-Hydroxytryptamine 4 receptor (5-HT4) (Serotonin receptor) (5-HT4).
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI.TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95317299; PubMed=7796807;
RA Gerald C., Adham N., Kao H.T., Olsen M.A., Laz T.M., Schechter L.E.,
RA Bard J.A., Vaysse P., Hartig P.R., Branchek T.A., Welnschank R.L.;
RT "The 5-HT4 receptor: molecular cloning and pharmacological
RT characterization of two splice variants.";
RL EMBO J. 14:2806-2815(1995).
RN [2]
RP SEQUENCE OF 165-259 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95385798; PubMed=7656980;
RA Ullmer C., Schumuck K., Kalkman H.O., Lubbert H.;
RT "Expression of serotonin receptor mRNAs in blood vessels.";
RL FEBS Lett. 370:215-221(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 5-HT4(E)).
RC TISSUE=Brain;
RX MEDLINE=99238795; PubMed=10220570;
RA Claeygen S., Sebben M., Becamel J.C., Bockaert J., Dumuis A.;
RT "Novel brain-specific 5-HT4 receptor splice variants show marked
RT constitutive activity: role of the C-terminal intracellular domain.";
RL Mol. Pharmacol. 55:910-920(1999).
CC -1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-
CC 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS
CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT STIMULATES ADENYLATE
CC CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing. Named isoforms=3;
CC Comment-Additional isoforms seem to exist;
CC Name=5-HT4L;
CC IsoId=Q62758-1; Sequence=Displayed;
CC Name=5-HT4S;
CC IsoId=Q62758-2; Sequence=VSP_001854;
CC Name=5-HT4(E);
CC IsoId=Q62758-3; Sequence=VSP_001855;
CC -1- TISSUE SPECIFICITY: IN BRAIN, THE 5-HT4S TRANSCRIPTS ARE
CC RESTRICTED TO THE STRIATUM, BUT THE 5-HT4L TRANSCRIPTS ARE
CC EXPRESSED THROUGHOUT THE BRAIN, EXCEPT IN THE CEREBELLUM. IN
CC PERIPHERAL TISSUES, DIFFERENTIAL EXPRESSION IS ALSO OBSERVED IN
CC THE ATRIUM OF THE HEART WHERE ONLY THE 5-HT4S ISOFORM IS
CC DETECTABLE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```


Query Match 24.2% Score 432.5 DB 1 Length 466:
Best Local Similarity 34.2% Pred. No. 2.8e-22:
Matches 120; Conservative 50; Mismatches 114; Indels 67; Gaps 122

QY	12	HPAFCQVNGSCPRVHTLGIQVLYITCAAGMLII-VLGNVFAVAFSYFKALHPT	69
DB	16	HPRA---QVN-----ISRAILLGLVLLGIIIGVAGNIIYLSVACHRIHSTV	61
QY	70	NEILLSLADLMFGLVLPLSTRSVSCFFGDFCLRLHTYDPLFCLSIHFICETIS	129
DB	62	HYVYIVLAVADLLTSPVLPESALFEILIGNAFAGVFCFNIMAWDYLCCTASIMGLCIIS	121
QY	130	IDRHCAICDPLLYESKFVRAVALRVLINAGVPAATSTLPLTDVVERLSQWLEMPV	189
DB	122	IDRIIGVSYPLRTPYIYQKRGVRLLCVW-----ALSLYISI--GPLEGWRQADPD	172
QY	190	GS-CQLLNKFKWGLNPEPL---FEPVCLIMISLYKIFVATRO-----AQ	231
DB	173	ETICO--INERGVYVLFALSGSEYPLIILVMCGRYVVAVKRESGLKSLGKTDKOSE	230
QY	232	QIT-----TLKSLAGAAKH-----EKRAKTLGIYVGIILCMPLPTI	270
DB	231	QVTLRIHKKNPVABGSGVSAKKNKTHFSVRLKFSREKRAKTLGIVGCEVLCMLPEPL	290
QY	271	DTWYDSL-HRTPEPLVDIIFWEAFYSACNPIIYVSQWFRALKTLT	320
DB	291	VMPGSGFPNNKRPPEYVFKIYFMWGLYNSCINPIIYPOSSQGEKKAQFNVL	341

RESULT 6
A1AA_RABIT STANDARD: PRT: 466 AA.

AC 002824;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97324192; PubMed=9180361;
RA Miyamoto S., Taniguchi T., Suzuki F., Takita M., Kosaka N., Negoro E., Okuda T., Kosaka H., Murata S., Nakamura S., Akagi Y., Oshita M., Watanabe Y., Muramatsu I.;
RT "Cloning, functional expression and tissue distribution of rabbit alpha1a-adrenoceptor";
RL Life Sci. 60:2069-2074(1997).
CC -I- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIN SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(O) AND G(11) PROTEINS.

```
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LIVER, VAS DEFERENS, BRAIN, AND AORTA, BUT NOT IN HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR HSSP; P02699; 1F8H.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00003; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 26 51 1 (POTENTIAL).
FT DOMAIN 52 63 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 64 89 2 (POTENTIAL).
FT DOMAIN 90 99 3 (POTENTIAL).
FT TRANSSEM 100 122 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 123 143 3 (POTENTIAL).
FT TRANSSEM 144 168 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 169 181 4 (POTENTIAL).
FT TRANSSEM 182 205 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 206 272 5 (POTENTIAL).
FT TRANSSEM 273 297 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 298 304 6 (POTENTIAL).
FT TRANSSEM 305 329 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 330 466 CYTOPLASMIC (POTENTIAL).
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAc...) (POTENTIAL).
SQ SEQUENCE 466 AA; 51365 MM; 9446D35B5DFCDEO CRC64;

Query Match 24.2% SCORE 432.5; DB 1; Length 466;
Best Local Similarity 33.2%; Fred. NO. 2.8e-22;
Matches 114; Conservative 53; Mismatches 121; Indels 55; Gaps 10.

QY 21 NGSCPRTVHTIGLDVIYTCAGAGLLI-VLGNVFAVAASYFKALTPNFILLSLAL 78
Db 11 SSNCTHPAPRNISKALLGVIIIGLLIFGVLGNLIIVLSVACHRHLSVTNYHVNLAV 70
QY 79 ADMELGLLVLPSTIRSVESCMFPQDPLCRHLTYIDLFCILSTPHLCFSIDRHCACID 138
Db 71 ADLLTLTSVFPEFSAIFELIGTWARGVCNMAVDVLTCSASTISLVIDRIDRGVSX 130
QY 139 PLTPSKRTVVVALRYITLAGMGVPAAYATSLDYDVET-RLSQMLEMPCGS-CQLLL 196
Db 131 PLRPFTIYTQRGRALCALCYVA-----FSLVISVGFLFGKRAPDDDTICQ--I 178
QY 197 NKFWGMNFPD--FEVPCLMISLYKFIFFVATRO-----AQQIT----- 234
Db 179 NEERGVLVSLAGSFYVBLTIILAMCVYVVVARRESGKLKSDKSDEQVTLRLHR 238
QY 235 ---TLSSISLAGAAH-----ERKAATLGIIVGTILYLCLMPFTIIDMWDSL 278
Db 239 KNAAGAGCGVASANKKTHFSVRLTKFSNEKRAATLGIIVGCFLVCLMFLVMPIGSFF 298
QY 279 HFTRPP-LVEDIFIMFAFNACNPDIIVFVSQYMRKALKTL 320
Db 299 PDFKPPEYVEKIVEMLGTLNSCINPIITPCSSQEKKAFQNVL 341
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ID	SHID_FUGRU	STANDARD:	PRT:	379 AA.
AC	P79746:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	5-hydroxytryptamine 1D receptor (5-HT-ID) (Seroctinin receptor) (5HTID) (FLD).			
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;			
OC	Tetraodontidae; Tetraodontidae; Takifugu.			
OX	NCBI_TaxId=31033:			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=97361762; PubMed=9218723;			
RA	Yamaguchi F., Brenner S.;			
RT	"Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor			
RL	genes from the Japanese puffer fish, Fugu rubripes.";			
CC	Genes 191:219-223(1997).			
CC	-1- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-			
CC	HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS			
CC	AS A NEUOTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF			
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE			
CC	CYCLASE ACTIVITY (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane prot:in.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	SYNOPSIS: TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb-sdb.ch).			
CC	-----			
DR	EMBL; X83865; CA58745.1; -			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHDOPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECPT_F2_1; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family.			
FT	DOMAIN 1	36		
FT	TRANSMEM 37	60		
FT	DOMAIN 61	73		
FT	TRANSMEM 74	96		
FT	DOMAIN 107	106		
FT	TRANSMEM 132	132		
FT	DOMAIN 133	152		
FT	TRANSMEM 153	174		
FT	DOMAIN 175	192		
FT	TRANSMEM 217	307		
FT	DOMAIN 308	331		
FT	TRANSMEM 332	339		
FT	TRANSMEM 340	364		
FT	DOMAIN 365	379		
FT	DISULFID 109	186		
FT	CARBOHYD 5	5		
FT	CARBOHYD 14	14		
FT	CARBOHYD 21	21		
SO	SEQUENCE 379 AA; 42301 MW; 99B6EC0379BEC78 CRC64;			
Query Match	23.7%;	Score 422.5;	DB 1	Length 379;
Best Local Similarity	30.8%;	Pred. No. 1.le-21;		
Matches 109;	Conservative 60;	Mismatches 108	Indels 77;	Gaps 10;

Db	33	LG6LQISVSVLAITYLTMTMTSNAFVLAITETFRKRLHPANPLIGSLAVTDMVLSILVPI	92
QY	91	STISVSGCWFEGDFLCRLHTFYLDTECLTIFHLICFISIDRHQACIDPLYPKSFYRV	150
Db	93	SIYTVTSKTSNGIYVCDIMSSDITICTASIIHLVYALADRYAITDALEYSKRRYMR	152
QY	151	ALRYILAGWGPAAVYSLFLTYTDYVERLSCMLEMPCVSGCOLLN---KFWGWLNF	206
Db	153	AAVAVAVVWVI-----SISIMSPLEFWHQAHAHELK-----ECGVNTDQISTYLYSPFG	202
QY	207	LEFPCLIMLSYKRIEVAFRQ-----AQQL-TLUSKL-----	240
Db	203	AFVYPTVLLIILYGRIVYAARSRIETKPPSYSGKRFTTAQLQTSAGSSICLSNSAND	262
QY	241	---AGA-----AKHKAATLIGIVGIIYLLCMLPF	268
Db	263	HLHSGAGEGGGSGFLPNSVAVKADNVLEKRLCLANERAKRTATLIGIILAFITTC	322
QY	269	TIDTMDVSLHFIIT-PPVEDIFITWFAVFNSSACNPIIY-VRS---YQWFRALK	317
Db	323	FVYTLVWNAICGCSFDPDLLFVFWIYGLNSLNPVIYITVYNDEKQAFOLIK	376

RESULT 8

ID	HH2R_CAVPO	STANDARD;	PRT;	359 AA.
AC	P47747;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Histamine H2 receptor (H2R) (gastric receptor 1).			
GN	HRH2.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.			
OX	NCBI_TaxID=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Hartley; TISSUE=Liver;			
RA	Traifort E;			
RL	Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC			
CC	ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G			
CC	PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U25440; AAA65713.1; -			
DR	PIR; JCA120; JCA120.			
DR	HSSP; P29274; IMMH.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHRDOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1.1; 1.			
DR	Protein; PS50262; G_PROTEIN_RECP_F1.2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 22			
FT	TRANSMEM 23 44			
FT	TRANSMEM 45 57			
FT	TRANSMEM 82 81			
FT	DOMAIN 88 92			
FT	TRANSMEM 93 114			
FT	DOMAIN 115 134			
FT	TRANSMEM 135 159			
FT	TRANSMEM 135 159			


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FT DOMAIN 160 180 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 181 204 5 (POTENTIAL).
FT DOMAIN 205 234 CYTOLASMIC (POTENTIAL).
FT TRANSSEM 235 258 6 (POTENTIAL).
FT DOMAIN 259 267 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 268 289 7 (POTENTIAL).
FT DOMAIN 290 359 CYTOLASMIC (POTENTIAL).
FT SITE 98 98 ESSENTIAL FOR HISTAMINE BINDING (BY SIMILARITY).
FT SITE 186 186 ESSENTIAL FOR TIOTIDINE BINDING AND IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
FT SITE 190 190 IMPLICATED IN HISTAMINE BINDING (BY SIMILARITY).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 91 174 BY SIMILARITY.
SO SEQUENCE 359 AA; 40556 MW; 58DB1BD8FC3C0E9 CRC64;

Query Match 23.5%; Score 420; DB 1; Length 359;
Best Local Similarity 33.1%; Pred. No. 1.6e-21;
Matches 103; Conservative 58; Mismatches 118; Indels 32; Gaps 10;

OY 21 NGSCPR-----TVHTLGIOLVYITLCAAGMLIIVGNFVAVSYFKALHTPTNELLS 75
DB 4 NGIVPSCMOTVYKVTISVILIL-----ILVTVAGNVVCLAGLNRLSLNCFIVS 59
OY 76 LALADMFGLVLPLSTIRSVESCFGDFLCRLHTYLDLFCLSIFHLCFISIDRCA 135
DB 60 LAVDLGLLVLPLFSAIYOLSCMSFSKVCNITYSLDYALCTASILNLFMISIDRCA 119
OY 136 ICDPLLPKRT-VRAVLRYLAWGVPAAATSLFLTYDVETRLSQMLEMPVGSOL 194
DB 120 VTDPLRPVLITPARVAISLVEI-WVI--STLSFLSLHLSMNSRNETSKNDITVCKV 176
OY 195 LNKFMGLN-FPLFEVPCILIMISLYKIEVAVATROAQOITLSLGAKEHKAAT 253
DB 177 QVNEVYGLVDSLVFVPLMLCMCTYFRIFKAREQARIHIG-SWMAATIRREKAVT 235
OY 254 LGIVVGYLACWLP-FIT-----DTMDSLHFTTPPLVEDIFTFVAVNSACNFI 304
DB 236 LAAMVGAFFICWFVEFVYVYRGKGDVAWEFE-----DVLMLGYANSALNPI 287
OY 305 YVFSYQWPKKA 315
DB 288 YALNRPFRFA 298

RESULT 9
ALAB_MESAU STANDARD; PRT: 515 AA.
ID ALAB_MESAU
AC P18841;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
GN ADRA1B.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89017157; PubMed=2845398;
RA Cotechia S., Schwinn D.A., Randall R.R., Lefkowitz R.J.,
RA Caron M.G., Kobilka B.K.;
RT "Molecular cloning and expression of the cDNA for the hamster alpha
RT 1-adrenergic receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 85:7159-7163(1988).
RX MEDLINE=92112850; PubMed=1346134;
RA Kjelberg M.A., Cotechia S., Ostrowski J., Caron M.G.,

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RA Lefkowitz R.J.;
RT "Constitutive activation of the alpha 1B-adrenergic receptor by all
RT amino acid substitutions at a single site. Evidence for a region
RT which constrains receptor activation."
RL J. Biol. Chem. 267:1430-1433(1992).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04084; AA58964.1; -.
DR PIR: A40491; A40491.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCR_RHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 46 70 1 (POTENTIAL).
FT DOMAIN 71 83 CYTOLASMIC (POTENTIAL).
FT TRANSSEM 84 105 2 (POTENTIAL).
FT DOMAIN 106 115 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 116 141 3 (POTENTIAL).
FT DOMAIN 142 161 CYTOLASMIC (POTENTIAL).
FT TRANSSEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 201 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 202 224 5 (POTENTIAL).
FT DOMAIN 225 295 CYTOLASMIC (POTENTIAL).
FT TRANSSEM 296 319 6 (POTENTIAL).
FT DOMAIN 320 326 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 327 340 7 (POTENTIAL).
FT DOMAIN 341 515 CYTOLASMIC (POTENTIAL).
FT TRANSSEM 371 378 POLY-ARG.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 118 195 BY SIMILARITY.
FT LIPID 365 365 PALMITATE (POTENTIAL).
FT MUTAGEN 293 A->X: CONFERS CONSTITUTIVE ACTIVITY.
SQ SEQUENCE 515 AA; 56492 MW; 6DAF1576D1CE3D CRC64;

Query Match 23.5%; Score 419; DB 1; Length 515;
Best Local Similarity 31.3%; Pred. No. 2.4e-21;
Matches 110; Conservative 54; Mismatches 135; Indels 52; Gaps 8;

OY 21 NGSCPRVHTLGIOLVYITLCAAGMLIIVGNFVAVSYFKALHTPTNELSLALAD 80
DB 34 NSTLPOLDVPAIS--VGLVIGAFILRAIVGNILIVSACNRLKRTPTNFYVNLAIAD 91
OY 81 MFDGLVLPSTIRSVESCFGDFLCRLHTYLDLFCLSIFHLCFISIDRCAICDPL 140
DB 92 LILSFYVLPFSATLEVGLVIGRIFEDIMAAVDVLCCTASISLCAISIDRYIGVRS 151
OY 141 LYPKFTVRAVLARKYLAWGVPAAATSLFLTYDVETRLSQMLEMPVGSOL 199
DB 152 QPPLVTRKATILALTSW-----VSTVISIGPLLGWKPAVDNDKECVTEBP 202
OY 200 WG-MLNPLPFPCLIMISLYKIFVAVATROAQI----- 233
DB 203 YALFSSIGSFYIPLAVILVMTCRVYIAKRTTKLNGVAKEMSKNELRLIRHSKNPHE 262

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QY 234 TTLSKSLAG-----AAK-----HERAAKTLGIVGITYLLCWLPTITDMVDSLH 280
 DB 263 DTLSTYKAGNPRSSIAVLEKFEKREKAATLGIYVGMFILCWLPTITDMVDSLH 322
 QY 281 ITPP-LVPDIFIMFAVNSACNPITYVSOMFRKALKLISQKVSPOQR 330
 DB 323 LKPPDAVFNVMELGTFNSCLNPIYPCSSKEFKRAFMRIJLQCCRSRRR 373

RESULT 10
 ALAA_CAVPO STANDARD: PRT; 466 AA.
 AC Q9W025;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-1a adrenergic receptor (Alpha 1a-adrenoceptor) (Alpha-1C adrenergic receptor).
 GN ADRA1A.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=21419075; PubMed=11527538;
 RA Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M., Gonzalez-Espinosa D., Garcia-Sainz J.A.;
 RT "Molecular cloning and functional expression of the guinea pig alpha(1a)-adrenoceptor".
 RL Eur. J. Pharmacol. 426:147-155(2001).
 CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
 CC AND G(11) PROTEINS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: AF108016; AAD22540.2; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 FT Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 25
 FT TRANSMEM 26 51
 FT DOMAIN 52 63
 FT TRANSMEM 64 89
 FT TRANSMEM 90 99
 FT TRANSMEM 100 122
 FT TRANSMEM 123 143
 FT TRANSMEM 144 168
 FT TRANSMEM 169 181
 FT TRANSMEM 182 205
 FT TRANSMEM 206 222
 FT TRANSMEM 223 297
 FT TRANSMEM 298 304
 FT TRANSMEM 305 329
 FT TRANSMEM 330 466
 FT LIPID 345 345
 FT CARBOHYD 7 7
 FT CARBOHYD 13 13

SQ SEQUENCE 466 AA; 51577 MW; E0E27EAFF5D30DCD CRC64;
 Query Match 23.4%; Score 418.5; DB 1; Length 466;
 Best Local Similarity 32.5%; Pred. No 2.4e-71;
 Matches 111; Conservative 54; Mismatches 124; Indels 53; Gaps 9;
 QY 21 NSGCPRTVHTLGIVLYITCAAGMLI--VLGNVFAVAVSFKALHPTNELLSLAL 78
 DB 11 SNNCTQPPAPVNIPIKAILLGVILGLILFCVGNPIILVILSVACHRHLSHTHYINLAV 70
 QY 79 ADMFGLVILPLSTISVESCFFGDFLCRLHYLTLCISIFHLCFSDIRCAICD 138
 DB 71 ADLLSTVLPFSALIEILGMAFGVFCINMAVAVLCTASIMISCTISIDRYGVSV 130
 QY 139 PLVPSKFWYRVAVRLITLGMGVPAVTSVLTVDVETRLSQMLEMPCVGS-COLLN 197
 DB 131 PLKFPVIVYORGLRALILCM-----ALSVYISI--GFLFGWRPAPODETICO--IN 179
 QY 198 KFWGMLNFPV---FVPCCLIMISLYVKIFVVAARQAQITTLKRS----- 239
 DB 180 EDRSVYLFSAIGSFYVPLAILIWMYCRVYVAVKRESGLTSGKTOKSDEQYTLRIHR 239
 QY 240 ---LAGAA-----KHEKAAKTLGIVGITYLLCWLPTITDMVDSLH 279
 DB 240 NAEPLGSSGVAASSKNKTHFSVRLKFSREKRAATLGIYVGCFLCWLPTITDMVDSLH 299
 QY 280 FTRP-PLVPDIFIMFAVNSACNPITYVSOMFRKALKLTL 320
 DB 300 DFKPSETVRIYVWLGILNSCLNPIYPCSSSEFKRAFQNVL 341

RESULT 11
 BLAR_XENLA STANDARD: PRT; 385 AA.
 ID BLAR_XENLA
 AC Q42574;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-1 adrenergic receptor (X-BETA1AR).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98055670; PubMed=9395292;
 RA Devic E., Faquereau L., Kagnad M., Steinberg R., Caput D., Audigier Y.;
 RT "Early expression of a beta1-adrenergic receptor and catecholamines in Xenopus oocytes and embryos".
 RL FEBS Lett. 417:184-190(1997).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: Y09213; CAAT0415.1; -
 DR HSSP: P07700; 1DEP.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECIP_F1.1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECIP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multiligand family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 38 61 1 (POTENTIAL).
FT DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 72 88 2 (POTENTIAL).
FT DOMAIN 89 109 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 110 131 3 (POTENTIAL).
FT DOMAIN 132 153 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 154 174 4 (POTENTIAL).
FT DOMAIN 175 200 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 201 223 5 (POTENTIAL).
FT DOMAIN 224 272 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 273 297 6 (POTENTIAL).
FT DOMAIN 298 303 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 304 326 7 (POTENTIAL).
FT DOMAIN 327 385 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 108 187 BY SIMILARITY.
FT LIPID 340 340 PALMITATE (BY SIMILARITY).
SO SEQUENCE 385 AA; 43309 MW; 0153D05A4E9EC1B CRC64;

Query Match 23.48; Score 418; DB 1; Length 385;
Beat Local Similarity 33.28; Pred. No. 2.2e-21;
Matches 109; Conservative 47; Mismatches 124; Indels 48; Gaps 9;

OY 25 PRTHV--TIGIQIYIYLTCAAGMLITVGNFVAFNAYFKALHTPPFLLSLADMF 82
DB 28 PELTHQMTGMTM---NAIILITVGNIMVVALGRNRLDTLTINVFITSLACALI 83
OY 83 LGLVLPSTIRSVESCFEGDFLCRLTYDTLFTCLTSIFHLCSIDRHCACDPLLY 142
DB 84 MGLFVPLGATLVYSGRLVGSIFCEFWTSVDVLCVASIEFLCVISIDRYATISPRY 143
OY 143 PSKRTVVALRYIAGMCPVPAVTSILPYTDVETRLSQMLE-----MPCV---GSCQ 193
DB 144 QSLITKGRAGKIVSWGISLVSFLP-----MMHWRDGDPLAMKCYEDPGCD 195
OY 194 LLLKFMQMLNFP--FEVPCLLIMISLVYKIFVATROAQI----- 233
DB 196 FVTRAVAIASISIFRPLIMFVYIRVFEKAKOKKIDKEGRSHSVLSHGSS 255
OY 234 -TTLSSKSLAGAKHERRAKTLGIVGVYLLCMLPFTIDVWDSLHETTPPLVDFITW 292
DB 256 RRIISKLIVA---KEOKALKTLGIIMGFLLCMLPFLANVNVFYRNLPDKLFLFLNW 312
OY 293 FAYENSACNPITVYFSQWFRKALKLTL 320
DB 313 LGVANSAPNPITVYCRSPD-FRKAKRRL 339

RESULT 12
ALAB_RAT ID ALAB_RAT STANDARD: PRT: 515 AA.
AC P15823; 063215;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alpha-1b adrenergic receptor (Alpha 1b-adrenoceptor).
GN ADRA1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=90192094; PubMed=2156222;
RA Voigt M.M., Kispert J., Chin H.;
RT "Sequence of a rat brain cDNA encoding an alpha-1b adrenergic

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RT receptor.";
RL Nucleic Acids Res. 18:1053-1053(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91177889; PubMed=1706716;
RA Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A.,
RA Yang-Feng T.L., Brownstein M., Leikowitz R.J., Caron M.G.;
RT "Molecular cloning and expression of the cDNA for the alpha 1A-
RT adrenergic receptor. The gene for which is located on human
RL chromosome 5.";
RL J. Biol. Chem. 266:6365-6369(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010315; PubMed=8406017;
RA Gao B., Kinos G.;
RT "Isolation and characterization of the gene encoding the rat alpha 1B
RT adrenergic receptor.";
RL Gene 131:243-247(1993).
RN [4]
RP SEQUENCE OF 1-253 FROM N.A.
RX MEDLINE=95081407; PubMed=7989580;
RA Kanasaki M., Matsubara H., Murasawa S., Masaki H., Mio Y., Inada M.;
RT "cAMP responsive element-mediated regulation of the gene
RT transcription of the alpha 1B adrenergic receptor by thyrotropin.";
RL J. Clin. Invest. 94:2245-2254(1994).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; X51585; CAAG35934.1; -.
DR EMBL; M60655; AAA63478.1; -.
DR EMBL; L08610; AAA40647.1; -.
DR EMBL; L08609; AAA40647.1; JOINED.
DR EMBL; D32045; BAA06806.1; -.
DR PIR; JC1525; JC1525.
DR HSSP; P29274; IMMH.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; G-PROTEIN_RECIP_F1.1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECIP_F1.1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECIP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multiligand family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 46 70 1 (POTENTIAL).
FT DOMAIN 71 83 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 84 105 2 (POTENTIAL).
FT DOMAIN 106 115 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 116 141 3 (POTENTIAL).
FT DOMAIN 142 161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 162 182 4 (POTENTIAL).
FT DOMAIN 183 201 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 202 224 5 (POTENTIAL).
FT DOMAIN 225 295 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 296 319 6 (POTENTIAL).
FT DOMAIN 320 326 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 327 340 7 (POTENTIAL).
FT DOMAIN 341 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 371 378 POLY-ARG.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 118 195 BY SIMILARITY.

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FT LIPID 365 365 PALMITATE (POTENTIAL).
FT CONFLICT 114 116 GRI -> LSF (IN REF. 2).
FT CONFLICT 203 203 Y -> C (IN REF. 1 AND 4).
FT CONFLICT 207 207 S -> C (IN REF. 1 AND 4).
FT CONFLICT 306 306 C -> S (IN REF. 3).
FT CONFLICT 415 416 TQ -> OK (IN REF. 1).
FT CONFLICT 440 440 C -> Y (IN REF. 3).
FT CONFLICT 484 486 GDT -> ATA (IN REF. 1).
FT CONFLICT 493 493 T -> S (IN REF. 3).
FT CONFLICT 511 511 A -> G (IN REF. 1).
SQ SEQUENCE 515 AA; 56585 MW; AF0C3759F80C3135 (RC64);

Query Match 23.4%; Score 418; DB 1; Length 515;
Best Local Similarity 31.8%; Pred. No. 2, 8e-21;
Matches 107; Conservative 52; Mismatches 125; Indels 52; Gaps 8;

OY 21 NSCSPTVHTLGLQVLYITCAAGMLIYGNVFAFAVYFRALHTPTNELLSTALND 80
DB 34 NSTLPLQDVYTRALS--VGLVLCGLFLEAIVGNILVLSV;CNHLPPTNYFTVNLAIAD 91
OY 81 MFLGLVLPSTIRSVESQWFGDFLCRLHTYLDLFLC;LSFHLCFISIDRCAICDPL 140
DB 92 LLSTFVLFPFSAFLVLELGYWVIGRIFCDIMANDVLCCT;SILSLCAISIDRIGVRSYL 151
OY 141 LYPSTFVVALRYIAGWGPAAVYSLFLYDVVETRL;QWLEEMPVCG-SCQLILNKF 199
DB 152 QPPTVTRRAKAILALISLV-----VLSTVVISIGPL;GMKEPAPNDKCEGVNEEPF 202
OY 200 WG-WTNFPLFEVPCLMISLVYKIFVATROAQI----- 233
DB 203 YALFSSLSGFYPLAVILWYCVYVARTKTNLAGV;KREMSNKELTLRISHNPFH 262
OY 234 TILSKSLAG-----AAK-----HERKAATLGIYGVLYLLCWLPTIDTWDSLHF 280
DB 263 DTLSSKAKGHNPRSSINAKLEFRSEKKAATLGIYGVLYLLCWLPTIDTWDSLHF 322
OY 281 TRPP-LVPDIFTFMAYFNSACNPIYVSYQMFRA 315
DB 323 LKPPDAVFKVFWGLGFGNSCLNPIIYPCSSKEFKRA 358

RESULT 13
ALIB_HUMAN STANDARD; PRT; 519 AA.
ID ALIB_HUMAN STANDARD; PRT; 519 AA.
AC P35368;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor).
GN ADRA1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=93016158; PubMed=1328250;
RA Ramarao C.S., Denker J.M., Perez D.M., Galvin R.J., Risk R.P.,
RA Graham R.M.;
RA "Genomic organization and expression of the human alpha 1B-adrenergic
RT receptor.";
RT J. Biol. Chem. 267:21936-21945(1992).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=94239386; PubMed=8183249;
RA Forray C., Bard J.A., Wetzel J.M., Chiu G., Shajiro E., Tang R.,
RA Lepor H., Hartig P.R., Weinschank R.L., Branchek T.A.,
RA Gluchowski C.;
RA "The alpha 1-adrenergic receptor that mediates smooth muscle
RT contraction in human prostate has the pharmacological properties of
RT the cloned human alpha 1c subtype.";
RL Mol. Pharmacol. 45:703-708(1994).

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RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwaun D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA Norman N.P., Campbell S., Fildock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues.";
RL J. Pharmacol. Exp. Ther. 272:134-142(1995).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M99589; -; NOT_ANNOTATED_CDS.
CC EMBL; M99590; -; NOT_ANNOTATED_CDS.
CC EMBL; U03865; AAB60352.1; -.
CC EMBL; L31773; AAB59485.1; -.
CC PIR; A45121; A45121.
CC HSSP; P28274; 1MMH.
CC GeneW; HGNC:278; ADRA1B.
CC MIM; 104220; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004937; F: alpha1-adrenergic receptor activity; TAS.
DR GO; GO:0008283; P: cell proliferation; TAS.
DR GO; GO:0007267; P: cell-cell signaling; TAS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signaling. . .; TAS.
DR GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleo. . .; TAS.
DR GO; GO:0007243; P: protein kinase cascade; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1.
DR PROSITE; PS50262; G-PROTEIN_RECP_F1_2_1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Palmitate.
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 45
FT TRANSMEM 46 70
FT DOMAIN 71 83
FT TRANSMEM 84 105
FT DOMAIN 106 115
FT TRANSMEM 116 141
FT DOMAIN 142 161
FT TRANSMEM 162 182
FT TRANSMEM 183 201
FT TRANSMEM 202 224
FT TRANSMEM 225 295
FT TRANSMEM 296 319
FT DOMAIN 320 326
FT TRANSMEM 327 340
FT DOMAIN 341 519
FT TRANSMEM 342 379
FT DOMAIN 370 379
FT CARBOHYD 10 10
FT CARBOHYD 24 24
FT CARBOHYD 29 29
FT CARBOHYD 34 34
FT DISULFID 118 195
FT LIPID 365 365
FT CONFLICT 370 370
FT CONFLICT 379 379
FT CONFLICT 497 500
SQ SEQUENCE 519 AA; 56778 MW; C4727A147D0A1780 CRC64;

```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92028990; PubMed=1930188;
 RA Ruat M., Traillfort E., Arrang J.-M., Leurs R., Schwartz J.-C.;
 RT Cloning and tissue expression of a rat histamine H2-receptor gene.;
 RL Biochem. Biophys. Res. Commun. 179:1470-1478(1991).
 CC -1- FUNCTION: THE H2 SUBCLASS OF HISTAMINE RECEPTORS MEDIATES GASTRIC
 ACID SECRETION. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
 PROTEINS WHICH ACTIVATE ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: S57565; AAB19935.1; -
 DR PIR: J01278; J01278.
 DR HSSP: P29274; 1MMH.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 FT DOMAIN 1 22
 FT TRANSMEM 23 44
 FT DOMAIN 45 57
 FT TRANSMEM 58 81
 FT DOMAIN 82 92
 FT TRANSMEM 93 114
 FT DOMAIN 115 134
 FT TRANSMEM 135 159
 FT DOMAIN 160 179
 FT TRANSMEM 180 203
 FT DOMAIN 204 233
 FT TRANSMEM 234 257
 FT DOMAIN 258 266
 FT TRANSMEM 267 288
 FT DOMAIN 289 358
 FT SITE 98 98
 FT SITE 185 185
 FT SITE 189 189
 FT SITE 189 189
 FT CARBOHYD 4 4
 FT DISULFID 91 173
 FT SEQUENCE 358 AA; 40253 MW; 4889F69B7B5D5DDC CRC64;
 SQ
 Query Match 23.3%; Score 416.5; DB 1; Length 358;
 Best Local Similarity 31.8%; Pred. No. 2, 7e-21;
 Matches 106; Conservative 53; Mismatches 127; Indels 47; Gaps 9;
 QY 27 TVH-----TLGIQVLYITLCAAGMLITVGNVFAFAV;YFKALHTPTNELLSLALAD 81
 DB 6 TVHSCDLSMALKVTISVLTLLITLITINGNVVCLAV;LNRRLRSITNCFIYSLATDL 65
 QY 82 FIGLIVLPSTIRSVSCWFEGLICRLTYISIDTLFCLISIFHLCTISIDRCACIDPDL 141
 DB 66 LIGLIVLPSPSAIYQISFTWSFGHVFNCNITYSIDVMLCT;SINLFWISIDRYCAVDPDL 125
 QY 142 YPSKFT-VEVALRYILAGWGVPAAYSLFYTQVETRI;SOMLEMPCVG-----SCOLL 195
 DB 126 YFVLVTPVAVAIISLVFI-WVISTLSFLSHLG-----WNSRNGTRGNDTFKCKVO 176

QY 196 LNFQWGLN-FPLEFVPCILIMISLYYKIFVATROAQOITLTSKSLAGAAHRRKAATL 254
 DB 177 VNEVYGLVDSGLVTFEYLPDLIMCTYYRIEFLAREQAKRIWHIS-SMKAATIRHKAFTVL 235
 QY 255 GIIVGYILQWLPF-----TIDTWDSLHFTYTPPLVEDIFITWAFYENSACN 301
 DB 236 AAVMGAFILICWPFYFAFYRGIRGDDALINEAVEG-----IVLMIGYANSALN 283
 QY 302 PIIVFSYQWFRKALTLTSQKVFSPQTRTVDL 334
 DB 284 PILYALNDRFRTAYOQLFHCKFASHNSHRTSL 316

Search completed: August 26, 2003, 14:24:11
 Job time : 15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:22:07 ; Search time: 40 Seconds

(without alignments)
2174.093 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785
Sequence: 1 KRAVFIGAEHPAFCYQV.....LTLSQKTPSPQRTVDLYGE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1785	100.0	337	4	014804	014804 homo sapien
2	843.5	47.3	344	11	0923X9	0923X9 rattus norv
3	836.5	46.9	344	11	0923Y3	0923Y3 rattus norv
4	836.5	46.9	358	11	0923Y1	0923Y1 rattus norv
5	830.5	46.5	358	11	0923Y2	0923Y2 rattus norv
6	825.5	46.2	344	11	0923Y0	0923Y0 rattus norv
7	815.5	45.7	343	11	0923X8	0923X8 rattus norv
8	812.5	45.5	348	4	096R19	096R19 homo sapien
9	808.5	45.3	358	11	0923X6	0923X6 rattus norv
10	805	45.1	345	11	0923Y5	0923Y5 rattus norv
11	802.5	45.0	358	11	0923X5	0923X5 rattus norv
12	797.5	44.7	358	11	0923Y4	0923Y4 rattus norv
13	795.5	44.6	338	11	0923Y6	0923Y6 rattus norv
14	786.5	44.1	345	4	096R18	096R18 homo sapien
15	785.5	44.0	342	4	096R14	096R14 homo sapien
16	744.5	41.7	362	11	0923X7	0923X7 rattus norv

17	740	41.5	347	11	0923Y7	0923Y7 rattus norv
18	696.5	39.0	306	4	09P1P5	09P1P5 homo sapien
19	678.5	38.0	338	6	08H264	08H264 macaca mula
20	677.5	38.0	339	4	096R20	096R20 homo sapien
21	674.5	37.8	343	4	09P1P4	09P1P4 homo sapien
22	657	36.8	332	11	0923Y8	0923Y8 mus musculu
23	623.5	34.9	332	11	08VH05	08VH05 mus musculu
24	617.5	34.6	332	11	0923Y9	0923Y9 rattus norv
25	498	27.9	328	13	09YH08	09YH08 rattus norv
26	489.5	27.4	352	13	09YH04	09YH04 fugu rubrip
27	489	27.4	328	13	09YH07	09YH07 fugu rubrip
28	484	27.1	353	13	09YH03	09YH03 lampetra fl
29	455.5	25.5	378	4	096KH9	096KH9 homo sapien
30	455.5	25.5	387	4	096KH0	096KH0 homo sapien
31	455.5	25.5	388	4	081KH9	081KH9 homo sapien
32	439.5	24.6	394	5	09NH03	09NH03 aplysia cal
33	435.5	24.4	508	5	09VC23	09VC23 drosophila
34	434.5	24.3	394	5	09NJS6	09NJS6 aplysia kur
35	432.5	24.2	425	6	09MZU2	09MZU2 oryctolagus
36	432.5	24.2	427	11	08BUE5	08BUE5 mus musculu
37	432.5	24.2	429	6	09MZU3	09MZU3 oryctolagus
38	432.5	24.2	466	11	08BV77	08BV77 mus musculu
39	424	23.8	518	6	09MY18	09MY18 oryctolagus
40	421.5	23.6	340	13	09YH02	09YH02 lampetra fl
41	418	23.4	459	11	08CG15	08CG15 mus musculu
42	418	23.4	515	11	09DB10	09DB10 mus musculu
43	414.5	23.2	466	4	096R08	096R08 homo sapien
44	413.5	23.2	358	11	090X37	090X37 mus musculu
45	413.5	23.2	397	11	09D282	09D282 mus musculu

ALIGNMENTS

RESULT 1
ID 014804
AC 014804; PRELIMINARY; PRT; 337 AA.
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Putative neurotransmitter receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98125534; PubMed=9464258;
RA Zeng Z., Fan P., Rand E., Kyaw H., Su K., Madlke V., Carter K.C.,
RA Li Y.;
RT "Cloning of a putative human neurotransmitter receptor expressed in
RT skeletal muscle and brain."
RL Biochem. Biophys. Res. Commun. 242:575-578(1998).
CC -1- SIMILARITY: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF021818; AAC39581.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000832; GPCR_secretin.
DR InterPro: IPR001917; NHRtransf_2.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCRHHODPSN.
DR PROSITE: PS00599; AA_TRANSF. CLASS 2; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_FL2; 1.
DR PROSITE: PS00261; G_PROTEIN_RECP_FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 337 AA; 38300 MW; 32134652B85CB35A CRC64;

Query Match 100.0%; Score 1785; DB 4; Length 337;
Best local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRAVFIGAEHPAFCYQVNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVS 60
DB 1 MRAVFIGAEHPAFCYQVNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVS 60
QY 61 YFKALHPPTNLLSLADMFGLVPLSTIRSVESCFEGRRLHTYLDLTLT 120
DB 61 YFKALHPPTNLLSLADMFGLVPLSTIRSVESCFEGRRLHTYLDLTLT 120
QY 121 SIFHLCEISIDRHCACDPLLPKFTVRALRYILAGWGPAAVTSLELYDVERRLS 180
DB 121 SIFHLCEISIDRHCACDPLLPKFTVRALRYILAGWGPAAVTSLELYDVERRLS 180
QY 181 QMLEEMPCVSCQILLKFMGMNPLFEVPCLLMISLYKIFVAVATROAOQITTLSSSL 240
DB 181 QMLEEMPCVSCQILLKFMGMNPLFEVPCLLMISLYKIFVAVATROAOQITTLSSSL 240
QY 241 AGAKHERKAKTIGIVGILLCMLPFTIDTMDSLHFTTPPLVEDIFIMFAVFNASC 300
DB 241 AGAKHERKAKTIGIVGILLCMLPFTIDTMDSLHFTTPPLVEDIFIMFAVFNASC 300
QY 301 NPIIVFSYQWFRKALKITLSQKVSPOTRTVLDLYOE 337
DB 301 NPIIVFSYQWFRKALKITLSQKVSPOTRTVLDLYOE 337

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RESULT 2

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QY 0923X9 PRELIMINARY; PRT; 374 AA.
AC 0923X9;
DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
DE Trace amine receptor 11.
GN Tail.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE-21374364; PubMed-11459929;
RA Borowaky B., Adam N., Jones K.A., Raddatz R., Artyomshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Licheblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: AF380199; AAK71250.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR000585; Hemopexin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
DR PROSITE: PS00024; HEMOPEXIN; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 374 AA; 41495 MW; C68FDE2D04AA7AB CRC64;

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Query Match 47.3%; Score 843.5; DB 11; Length 374;
 Best Local Similarity 45.8%; Pred. No. 6.7e-66;
 Matches 154; Conservative 68; Mismatches 103; Indels 11; Gaps 2;

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QY 13 PAACFYQ-VNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVSFKALHTPTNF 71
DB 39 PLQCYEVNVAASCKITPYSPGLRYLVLPVFGFVAVLAVCGMLLVIVSLHFKOLHSPANF 98
QY 72 LLASDLADMFGLVPLSTIRSVESCFEGRRLHTYLDLTLTFCSTSFHLCFTSID 131
DB 99 LLASDLADMFGLVPLSTIRSVESCFEGRRLHTYLDLTLTFCSTSFHLCFTSID 158

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QY 132 RHCAICDPLLPKFTVRALRYILAGWGPAAVTSLELYDVERRLSOMLEEMPCVS 191
DB 159 RYIAVTDPLVPKFTVSVSGICISIMILPLVSSAVFTGATGICENLVSLNCGV 218
QY 192 COLLKFMGMNPLFEVPCLLMISLYKIFVAVATROAOQITTLSSSL 241
DB 219 CQIVNDWVLDLPLIPVIMILSKFLVAKOAVKIFETISGSGESSLESKHA 278
QY 242 GAHERKAKTIGIVGILLCMLPFTIDTMDSLHFTTPPLVEDIFIMFAVFNASC 301
DB 279 RVAKHERKAKTIGIVGILLCMLPFTIDTMDSLHFTTPPLVEDIFIMFAVFNASC 338
QY 302 PIIVFSYQWFRKALKITLSQKVSPOTRTVLDLYOE 337
DB 339 PLIVAFYQWFRKALKITLSQKVSPOTRTVLDLYOE 374

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RESULT 3

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QY 0923Y3 PRELIMINARY; PRT; 344 AA.
AC 0923Y3;
DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel, 23, Last annotation update)
DE Trace amine receptor 7.
GN Tail.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE-21374364; PubMed-11459929;
RA Borowaky B., Adam N., Jones K.A., Raddatz R., Artyomshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Licheblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: AF380195; AAK71246.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR000585; Hemopexin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEPTOR_F1_2; 1.
DR PROSITE: PS00024; HEMOPEXIN; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 344 AA; 38043 MW; 45C41C861E5F6408 CRC64;

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Query Match 46.9%; Score 836.5; DB 11; Length 344;
 Best Local Similarity 46.1%; Pred. No. 2.5e-65;
 Matches 153; Conservative 67; Mismatches 101; Indels 11; Gaps 2;

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QY 17 CYQ-VNGSCPRTVHTIGIQLVITLCAAGMLIIVLGAVFAVAVSFKALHTPTNF 75
DB 13 CYENVAASCKITPYSPGLRYLVLPVFGFVAVLAVCGMLLVIVSLHFKOLHSPANF 72
QY 76 LALDMFGLVPLSTIRSVESCFEGRRLHTYLDLTLTFCSTSFHLCFTSIDRHA 135
DB 73 LASADFLVGSIVMFPNSVRSIESCWYGDTPFCSLHSCDAFCSLFLHLCFTSIDRHA 132
QY 136 ICDPLLPKFTVRALRYILAGWGPAAVTSLELYDVERRLSOMLEEMPCVSCQL 195
DB 133 VTEPLVPKFTVSVSGICISIMILPLVSSAVFTGATGICENLVSLNCGV 192
QY 196 LNKFMGMNPLFEVPCLLMISLYKIFVAVATROAOQITTLSSSL 245

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Db      193 INQDWLISFLFPIPLVMIILSKIFLVAKQAVKIETISIGSGESSLESHKARYAK 252
QY      246 HERKAKTIGIVGIIYLLCWLPEFTIDPMWDSILHFTTPPIVDIDITMFAVENSACNPITY 305
Db      253 RRRKAKTIGIVTVMFVMSWMLPYTIDTLDAFMGFTTPAVYELGCMIAVYNSAMPITY 312
QY      306 VPSYQWFRKAKLTLSQKVFSPQTRVDLYOE 337
Db      313 AFYFWRKAKILITLISGKILKHSSTLSLFE 344

RESULT 4
0923Y1 PRELIMINARY; PRT; 358 AA.
AC      0923Y1;
DT      01-DEC-2001 (TREMblrel. 19, Created)
DT      01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE      Trace amine receptor 9.
GN      TAG.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Sprague-Dawley;
RX      MEDLINE=21374364; PubMed=11459929;
RA      Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
RA      Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA      Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA      Branchek T.A., Gerald C.;
RT      "Trace amines: Identification of a family of mammalian G protein-
RT      coupled receptors."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL: AF380197; AAK71248.1;
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm.1. 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR      PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
SQ      SEQUENCE 358 AA; 39962 MW; 0B392B5C312AE8A3 JRC64;

Query Match      46.9%; Score 836.5; DB 11; Length 358;
Best Local Similarity 45.5%; Pred. No. 2,6e-65;
Matches 150; Conservative 70; Mismatches 101; Indels 9; Gaps 2;

QY      17 CYQ-VNGSCPRTVHTLGIQIYIYLTCAAGMLIIVGNVFAVAVSYFKALHTPTNELL 75
Db      29 CYENLNSCVSPSPSRLIYAVFGFAVLAVCGNMLVMTSLHFRQLHSPANFLVAS 88
QY      76 LALADMLGLIYLPSTISVSCWFGDFLCRIHTYIDLTCFLTSIFHLCEFSIDRHA 135
Db      89 LACADLVGLTVMPFSVMSRVEGCMYFGDSCYKLSCHPDISFGSSSLHLCFISVDRIA 148
QY      136 ICDPLIYPSKFTVRVALRYILAGWGPAAVTSFLYTDVETRLSOMLEMPCVSGCOLL 195
Db      149 VSDPLIYPTRTASVSGKITIFSWLSITIFGSLIYTGASAGLEDVLSALTVCVGCQVA 208
QY      196 LAKFWGMLNPLFPVPCILMISLYKIFVAVTRAOQITLTSKSLAGA-----AKHE 247
Db      209 VNGSWFENFLPFLVPAVMTVYSKIFLAKQAOANNEKMSKQTAARSIDSKDRAKRE 268
QY      248 RKAATIGIVGIIYLLCWLPEFTIDPMWDSILHFTTPPIVDIDITMFAVENSACNPITY 307
Db      269 RKAATIGIVAAFLSLMLPYVDSIIDALGFTITPTVYIELAMIAVYNSAMPITYAF 328
QY      308 SYQWFRKAKLTLSQKVFSPQTRVDLYOE 337
Db      329 FYFWRKAKILITLISGKILKHSSTLSLFE 358

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RESULT 5
0923Y2 PRELIMINARY; PRT; 358 AA.
AC      0923Y2;
DT      01-DEC-2001 (TREMblrel. 19, Created)
DT      01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE      Trace amine receptor 8.
GN      TAG.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Sprague-Dawley;
RX      MEDLINE=21374364; PubMed=11459929;
RA      Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
RA      Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA      Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA      Branchek T.A., Gerald C.;
RT      "Trace amines: Identification of a family of mammalian G protein-
RT      coupled receptors."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL: AF380196; AAK71247.1;
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm.1. 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR      PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
SQ      SEQUENCE 358 AA; 40146 MW; E136ADA32C1A268B CRC64;

Query Match      46.5%; Score 830.5; DB 11; Length 358;
Best Local Similarity 45.8%; Pred. No. 8,8e-65;
Matches 151; Conservative 68; Mismatches 102; Indels 9; Gaps 2;

QY      17 CYQ-VNGSCPRTVHTLGIQIYIYLTCAAGMLIIVGNVFAVAVSYFKALHTPTNELL 75
Db      29 CYENLNSCVSPSPSRLIYAVFGFAVLAVCGNMLVMTSLHFRQLHSPANFLVAS 88
QY      76 LALADMLGLIYLPSTISVSCWFGDFLCRIHTYIDLTCFLTSIFHLCEFSIDRHA 135
Db      89 LACADLVGLTVMPFSVMSRVEGCMYFGDSCYKLSCHPDISFGSSSLHLCFISVDRIA 148
QY      136 ICDPLIYPSKFTVRVALRYILAGWGPAAVTSFLYTDVETRLSOMLEMPCVSGCOLL 195
Db      149 VSDPLIYPTRTASVSGKITIFSWLSITIFGSLIYTGANAGLEDVLSALTVCVGCQVA 208
QY      196 LAKFWGMLNPLFPVPCILMISLYKIFVAVTRAOQITLTSKSLAGA-----AKHE 247
Db      209 VNGSWFENFLPFLVPAVMTVYSKIFLAKQAOANNEKMSKQTAARSIDSKDRAKRE 268
QY      248 RKAATIGIVGIIYLLCWLPEFTIDPMWDSILHFTTPPIVDIDITMFAVENSACNPITY 307
Db      269 RKAATIGIVAAFLSLMLPYVDSIIDALGFTITPTVYIELAMIAVYNSAMPITYAF 328
QY      308 SYQWFRKAKLTLSQKVFSPQTRVDLYOE 337
Db      329 FYFWRKAKILITLISGKILKHSSTLSLFE 358

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Query Match	46.28;	Score 825.5;	DB 11;	Length 344;
Best Local Similarity	45.88;	Pred. NO. 2.3e-64;		
Matches 152;	Conservative 65;	Mismatches 104;	Indels 11;	Gaps 2

RP SEQUENCE FROM N.A.

Query Match	45.78;	Score 815.5;	DB 11;	Length 333;
Best Local Similarity	44.88;	Pred. No. 1.7e-63;		
Matches 148;	Conservative 67;	Mismatches 106;	Indels 9;	Gaps 2;

RESULT 8	
Q96R19	
ID Q96R19	
PRELIMINARY;	
PRT;	348 AA.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)


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QY 64 ALHPTNFFLLSLALADMFGLVLPSTIRSVESCFEGDLCRLHTYDLECLNSIF 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 QLSHPTFFLLASLACAPFWGVSVMPFSMRSIESCHVFGSRFCTPHCCVACYSLEF 121
QY 124 HLCSTIDRHCATDPLLYSKFTVVALRYTLAGCVPAAYTSLELYDVERLSQWL 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 122 HLSTISIDRYLAVNDPLVYPTKFTSVSGICISISWMLPLAYSGAVFTGTAGGLEVS 181
QY 184 EEMCVGSCOLLKFKFQGNLPLFPVPCILIMISLYKIFVAVTRAOQITTLKSL--- 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 182 DAVNCVGGCVVAVNNWNLIDFLSFLIPTLVMILLKGFILVLAQOAKKIFETVGNKASS 241
QY 241 ----AGAAKHKRAKTLGIVGIIYLLCMLPFTIDVDSLHFTTPPLVDFIIFW 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 242 SESYKARVARRERKAATKLTITVAVFMISMLPSIDSLVDAFMGFTFPAYIYECW 301
QY 296 FNSACNPIIYFVSQWFRKAKLTLKSVESFQTRVDLYOE 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 302 YNSAMNPLIYALFYPMFKAKIYMSQVFNSSATMNLFS 343

RESULT 11
Q923X5 PRELIMINARY; PRT; 358 AA.
AC 0923X5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Trace amine receptor 15.
GN TA15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF380203; AAK71254.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40652 MW; EEBB4D9219EE1171 CRC64;

Query Match 45.0%; Score 802.5; DB 11; Length 358;
Best Local Similarity 44.8%; Pred. NO. 2.5e-62;
Matches 148; Conservative 67; Mismatches 106; Indels 9; Gaps 2;
QY 17 CYQ-VNGSCPRTVHTLGIOIYIYLTCAAGMLIYLVGNFVAVFYKALHPTNFFLLS 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 CYENINRSCVSPSPGRRLIYAVFGGAVLAVCGNLMVMTSLHFRQLHSPANFLVAS 88
QY 76 LALADMFGLVLPSTIRSVESCFEGDLCRLHTYDLECLNSIFHLCEISIDRCA 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 LACADLVGLVMPSPSVRSVSGCYFGDYCKLHTCDVSCYSLFHLCEISIDRYIA 148
QY 136 ICDPLLYSKFTVVALRYTLAGCVPAAYTSLELYDVERLSQWL EEMCVGSCOLL 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 149 VSDPLIYIRRTASVSGKICITFSMFLSIYGPPLIYTGASBAGLKDVLSCVGGCQIP 208
QY 196 LKRFQGNLPLFPVPCILIMISLYKIFVAVTRAOQITTLKSLAGAA-----KHE 247

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DB 209 MNQKFLVINFLEFLVPLVMMTVSKIFLARQOQNIKKRKQFARASSSYKDRVCKRE 268
QY 248 RKAATKGIYVIGIYLLCMLPFTIDVDSLHFTTPPLVDFIIFWAFNSACNPIIYVF 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 269 RKAATKGIYVAVLPLVMTVSKIFLARQOQNIKKRKQFARASSSYKDRVCKRE 328
QY 308 SYQWFRKAKLTLKSVESFQTRVDLYOE 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 FYPMFRKAKIYVTKLIRENSSTINLPE 358

RESULT 12
Q923Y4 PRELIMINARY; PRT; 358 AA.
AC 0923Y4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Trace amine receptor 6.
GN TA6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF380194; AAK71245.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 40074 MW; CAE028CF9943DCE CRC64;

Query Match 44.7%; Score 797.5; DB 11; Length 358;
Best Local Similarity 44.2%; Pred. NO. 6.8e-62;
Matches 146; Conservative 67; Mismatches 108; Indels 9; Gaps 2;
QY 17 CYQ-VNGSCPRTVHTLGIOIYIYLTCAAGMLIYLVGNFVAVFYKALHPTNFFLLS 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 CYENINRSCVSPSPGRRLIYAVFGGAVLAVCGNLMVMTSLHFRQLHSPANFLVAS 88
QY 76 LALADMFGLVLPSTIRSVESCFEGDLCRLHTYDLECLNSIFHLCEISIDRCA 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 89 LACADLVGLVMPSPSVRSVSGCYFGDYCKLHTCDVSCYSLFHLCEISIDRYIA 148
QY 136 ICDPLLYSKFTVVALRYTLAGCVPAAYTSLELYDVERLSQWL EEMCVGSCOLL 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 149 VSDPLIYIRRTASVSGKICITFSMFLSIYGPPLIYTGASBAGLKDVLSCVGGCQIP 208
QY 196 LKRFQGNLPLFPVPCILIMISLYKIFVAVTRAOQITTLKSLAGAA-----KHE 247
QY 209 MNQKFLVINFLEFLVPLVMMTVSKIFLARQOQNIKKRKQFARASSSYKDRVCKRE 268
QY 248 RKAATKGIYVIGIYLLCMLPFTIDVDSLHFTTPPLVDFIIFWAFNSACNPIIYVF 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 269 RKAATKGIYVAVLPLVMTVSKIFLARQOQNIKKRKQFARASSSYKDRVCKRE 328
QY 308 SYQWFRKAKLTLKSVESFQTRVDLYOE 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 329 FYPMFRKAKIYVTKLIRENSSTINLPE 358

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RESULT 13
ID 0923Y6 PRELIMINARY; PRT; 338 AA.
AC 0923Y6:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Trace amine receptor 3.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
RA Ogazalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380190; AAK71241.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1;
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 338 AA; 37846 MW; F8BC058A21664EA4 C1C64;

Query Match 44.6%; Score 795.5; DB 11; Length 338;
Best Local Similarity 45.5%; Pred. No. 9.7e-62;
Matches 150; Conservative 64; Mismatches 107; Indels 9; Gaps 3;

QY 17 CYQ-VNGSCPRVHTGIOLVITLTCACAGMLIVGNVAVFAVSFKALHTPTNLLLS 75
DB 4 CEENNGSCIKSSYSPWPAIIAYLGLALVAGLALVGNLVAITLHFKOLHPTNPLVAS 63
QY 76 LALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDPLCLTSIFHLCFISIDRCA 135
DB 64 LACADFLVGVVAFMSVTSVSGVYEGDFYCKFHCFDTCFQASLFLHLCISIDRYA 123
QY 136 ICDDPLLPKSFYRVARLRIIAGMGVPAAYTSLFLTYDVTIRLSOMLEEMPCVSGQL 195
DB 124 VTDPLVTPKFTISVSGVIALSWFSPVSYSTFYTGANIEGIELVVALTCVGGCQAP 183
QY 196 LKRFMGWLNFPLEFVPCILIMISLYKIFVAVTRQAQOI-TLSKSLAGA-----AKHE 247
DB 184 LNQNVVLLCFLEFLPYVAVFLYGRIFLVAQAKIDG;ANQOASESESKERAYARE 243
QY 248 RKAATLTGIVGIIYLCWLPFTIDVDSLHFTTPPLVEITFIWFAYNSACNPLIYF 307
DB 244 RKAATLTGIVAAAFVSMPLPYIDAVYNNFTIPAYVEITLVAVYNSAMNPLIYAF 303
QY 308 SYQWFRKALKLTLSOKVSPQRTVDLYOE 337
DB 304 FYWFRKAIKLVISGVKVRADSSRNLFSE 333

RESULT 14
ID 096R18 PRELIMINARY; PRT; 345 AA.
AC 096R18:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)

DE Trace amine receptor 4.
GN TA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artyushyn R.,
RA Ogazalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380192; AAK71243.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1.1
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1;
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 345 AA; 38451 MW; 21B1C4968C39F22C CRC64;

Query Match 44.1%; Score 786.5; DB 4; Length 345;
Best Local Similarity 44.2%; Pred. No. 6.1e-61;
Matches 146; Conservative 70; Mismatches 105; Indels 9; Gaps 3;

QY 17 CYQ-VNGSCPRVHTGIOLVITLTCACAGMLIVGNVAVFAVSFKALHTPTNLLLS 75
DB 14 CEANVNGSCVKIPFSGSRVILIVYFGAVLAVFENLVMISILFHKOLHPTNPLVAS 73
QY 76 LALADMFGLVLPSTIRSVESCFEGDFLCRLHTYDPLCLTSIFHLCFISIDRCA 135
DB 74 LACADFLVGVVAFMSVTSVSGVYEGDFYCKFHCFDTCFQASLFLHLCISIDRYA 133
QY 136 ICDDPLLPKSFYRVARLRIIAGMGVPAAYTSLFLTYDVTIRLSOMLEEMPCVSGQL 195
DB 134 VTDPLVTPKFTISVSGVIALSWFSPVSYSTFYTGANIEGIELVVALTCVGGCQAP 193
QY 196 LKRFMGWLNFPLEFVPCILIMISLYKIFVAVTRQAQOI-TLSKSLAGA-----LAGAKHE 247
DB 194 VNQNVVLLCFLEFLPYVAVFLYGRIFLVAQAKIDG;ANQOASESESKERAYARE 253
QY 248 RKAATLTGIVGIIYLCWLPFTIDVDSLHFTTPPLVEITFIWFAYNSACNPLIYF 307
DB 254 RKAATLTGIVAAAFVSMPLPYIDAVYNNFTIPAYVEITLVAVYNSAMNPLIYAF 313
QY 308 SYQWFRKALKLTLSOKVSPQRTVDLYOE 337
DB 314 FYWFRKAIKLVISGVKVRADSSRNLFSE 343

RESULT 15
ID 0969N4 PRELIMINARY; PRT; 342 AA.
AC 0969N4:
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE G protein-coupled receptor (Trace amine receptor 5).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
KW Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantli W.B., Arkhltko O.,

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OM protein - protein search, using sw model

Run on: August 26, 2003, 14:23:57 ; Search time 20 Seconds
(without alignments)
712.938 Million cell updates/sec

Title: US-09-988-745-2

Perfect score: 1785
Sequence: 1 MRAVFIOGAHEHPAAFCYGV.....LFLSQVFSPQRTVDLYOE 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:.*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/beckfile1.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	337	2	US-08-467-559B-2
2	812.5	45.5	348	3	US-09-286-805-2
3	793.5	44.6	338	3	US-09-286-805-4
4	674.5	37.8	343	2	US-08-788-539A-2
5	455.5	25.5	360	4	US-09-555-113B-4
6	455.5	25.5	380	4	US-09-555-113B-24
7	455.5	25.5	388	4	US-08-446-822-8
8	455.5	25.5	388	4	US-09-328-314-8
9	453.5	25.5	388	5	PCT-US93-12586-8
10	453.5	25.5	760	4	US-09-555-113B-2
11	446.5	25.0	387	1	US-07-996-772A-2
12	446.5	25.0	387	1	US-08-446-822-2
13	446.5	25.0	387	5	US-09-328-314-2
14	446.5	25.0	387	5	PCT-US93-12586-2
15	446.5	25.0	406	4	US-09-328-314-4
16	444.5	24.9	406	1	US-07-996-772A-4
17	444.5	24.9	406	1	US-08-446-822-4
18	444.5	24.9	406	5	PCT-US93-12586-4
19	420	23.5	359	5	US-08-748-485-5
20	419	23.5	513	2	US-08-406-855A-21
21	419	23.5	513	3	US-09-206-899-21
22	419	23.5	515	1	US-08-444-734A-7
23	419	23.5	515	2	US-08-406-855A-22
24	419	23.5	515	2	US-09-206-899-22
25	419	23.5	515	4	US-09-688-415-9
26	419	23.5	515	4	US-09-688-415-10
27	418	23.4	515	1	US-08-722-001-25

28	418	23.4	517	2	US-08-467-568-10	Sequence 10, Appl
29	418	23.4	517	2	US-09-030-582-10	Sequence 10, Appl
30	418	23.4	520	1	US-08-334-898-4	Sequence 4, Appl
31	418	23.4	520	1	US-08-228-932-4	Sequence 4, Appl
32	418	23.4	520	1	US-08-468-939-4	Sequence 4, Appl
33	418	23.4	520	2	US-08-406-855A-4	Sequence 4, Appl
34	418	23.4	520	2	US-08-722-190-4	Sequence 4, Appl
35	418	23.4	520	3	US-08-244-354-4	Sequence 4, Appl
36	418	23.4	520	3	US-09-206-899-4	Sequence 4, Appl
37	418	23.4	520	4	US-09-444-783-4	Sequence 4, Appl
38	418	23.4	520	4	US-09-688-415-4	Sequence 4, Appl
39	418	23.4	520	5	PCT-US95-04203-4	Sequence 4, Appl
40	416.5	23.3	358	2	US-08-748-485-6	Sequence 6, Appl
41	416	23.3	515	3	US-09-032-742-5	Sequence 5, Appl
42	415.5	23.3	359	2	US-08-467-568-13	Sequence 13, Appl
43	415.5	23.3	359	2	US-08-748-485-4	Sequence 4, Appl
44	415.5	23.3	359	2	US-08-103-170-2	Sequence 2, Appl
45	415.5	23.3	359	2	US-09-030-582-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-08-467-559B-2
: Sequence 2, Application US/08467559B
: Patent No. 5928890
: GENERAL INFORMATION:
: APPLICANT: LI, YI
: TITLE OF INVENTION: HUMAN AMINE RECEPTOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/467,559B
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: STEFFE, ERIC K
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488, 0840000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 371-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 337 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-467-559B-2

Query Match      100.0%; Score 1785; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.6e-143;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRAVFIOGAHEHPAAFCYGVNSCPRTVHTIGIQLVYITLCAAGMLITVGNFVAFAVS 60
        |||||||
DB      1 MRAVFIOGAHEHPAAFCYGVNSCPRTVHTIGIQLVYITLCAAGMLITVGNFVAFAVS 60
        |||||||

QY      61 YFAALHTPTNFFLLSLALADMFGLVLPSTIRSVESCFPFDDFLCRHTVYDPLFCLT 120
        |||||||
DB      61 YFAALHTPTNFFLLSLALADMFGLVLPSTIRSVESCFPFDDFLCRHTVYDPLFCLT 120
        |||||||
```

Oy	121	SIFHCFSIDBHCACIDCPILPKSFKEFVAVARILAGGCVPAAYSLFETPDYVEERBS	180
Db	121	SIFHCFSIDBHCACIDCPILPKSFKEFVAVARILAGGCVPAAYSLFETPDYVEERBS	180
Oy	181	QWLEBMPCVSGQCLLLNKFWMGLNPELPFCPLIMISLVKIFVVVATROAQOITTLTSL	240
Db	181	QWLEBMPCVSGQCLLLNKFWMGLNPELPFCPLIMISLVKIFVVATROAQOITTLTSL	240
Oy	241	AGAAHKEKAAKTLGIVGIYILCMLPFTIDIMWDSLHFTPPLVEDIFIMFAYNSAC	300
Db	241	AGAAHKEKAAKTLGIVGIYILCMLPFTIDIMWDSLHFTPPLVEDIFIMFAYNSAC	300
Oy	301	NPITIVFSYOMPRKALKLTLISQKVSPORTIYDLVQE	337
Db	301	NPITIVFSYOMPRKALKLTLISQKVSPORTIYDLVQE	337

```

RESULT 2
US-09-286-805-2
: Sequence 2, Application US/09286805
: Patent No. 6117990
: GENERAL INFORMATION:
: APPLICANT: Bonini, James A.
: APPLICANT: Borowsky, Beth E.
: TITLE OF INVENTION: DNA Encoding Orphan SNORF1 Receptor
: FILE REFERENCE: 58987
: CURRENT APPLICATION NUMBER: US/09/286.805
: CURRENT FILING DATE: 1999-04-06
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0 - beta
: SEQ ID NO. 2
: LENGTH: 348
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-286-805-2

```

Query Match	Similarity	45.5%	Score	812.5	DB	3	length	348:
Best Local	Similarity	46.1%	Pred.	2.8e-61				
Matches	152:	Conservative	64:	Mismatches	105:	Indels	9:	Gaps
QY	17	CYQ-VNGSCPRVTWHLGIQVLVYLTCAGAMLTIVIGANFVAFVSKALHTPTNFFLLS	75					
DB	14	CYKNVNESCIPTMPSPGPRSLIVAVLGRGAVLAAAGNLLVMALLHFKQLHTPTNFFLLAS	73					
QY	76	LALADMETGLVLPVLPSTIRSVESCSGFGDFLCRLHTYLDLTLECLTSIFHLCTSIDRCHA	135					
DB	74	LACADELGVVYTMPEPSTVRSVESCWYFSDSYCKEFTFCEDTSCFASLFFHLCTISVDRYIA	133					
QY	136	ICDPLLYSKFVVRALRYLLAGMGVPAAYTSLFYTVDVERNLSOMLEEMPCVSGCOLL	195					
DB	134	VTDLPTPTTKFTVASGICIVLSMFPSTVYSISITFYGANBERGIEELVVALTCVGGCQMP	193					
QY	196	LNKFWGMNLNPLFEVYPCILMISLVYKIFVAVAFRAQOI-TTLEKSLAGA-----AKHE	247					
DB	194	LNGNNVLLCLFLFFIPNVAMVFIYSKIFELVMAHQARKIESTASQAOSSESEYKERVAKRE	253					
QY	248	RKAATLGIVVGIYLLCMLPFTITMDVSLHFTHTPRLVYEDIFIMFAYFNSACNPIIYF	307					
DB	254	RKAATLTGIAMAEFLVSMPLVLDVDAVIDAYNMFTIPPVYETILVWCYVYNSAMNPIIYAF	313					
QY	308	SYOWFRKALKLTLISOKVFSPPQRYVDVQOE	337					
DB	314	FYQWFGKAIKLIVSGKVLRTDSTTNLSE	343					

RESULT 3
US-09-286-805-4
; Sequence 4, Application US/09286805
; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.

[illegible]

1 RESULT 4
 2 US-08-788-539A-2
 3 Sequence 2, Application US/08788539A
 4 Patent No. 5871967
 5
 6 GENERAL INFORMATION:
 7 APPLICANT: Smithkline Beecham Corporation
 8 TITLE OF INVENTION: CLONING OF A NOVEL G-PROTEIN
 9 TITLE OF INVENTION: COUPLED 7TM RECEPTOR
 10 NUMBER OF SEQUENCES: 2
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESS: Smithkline Beecham Corporation
 13 STREET: 709 Swedeland Road
 14 CITY: King of Prussia
 15 STATE: PA
 16
 17 COUNTRY: USA
 18
 19 ZIP: 19406
 20
 21 COMPUTER READABLE FORM:
 22 MEDIUM TYPE: Diskette
 23 COMPUTER: IBM Compatible
 24 OPERATING SYSTEM: DOS
 25 SOFTWARE: FASTSED for Windows Version 2.0
 26
 27 CURRENT APPLICATION DATA:
 28 APPLICATION NUMBER: US/08/788,539A
 29 FILING DATE: 24-JAN-1997
 30 CLASSIFICATION: 435
 31 PRIOR APPLICATION DATA:
 32 APPLICATION NUMBER:
 33 FILING DATE:
 34 ATTORNEY/AGENT INFORMATION:
 35 NAME: Han, William T
 36 REGISTRATION NUMBER: 34,344
 37 REFERENCE/DOCKET NUMBER: ATG50047


```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-788-539A-2

Query Match      37.8%; Score 674.5; DB 2; Length 343;
Best Local Similarity 39.4%; Pred. No. 1.3e-49;
Matches 130; Conservative 65; Mismatches 120; Indels 15; Gaps 3;

QY 23 SCPRVHTGIGIOLVITCAAGMLI-----IYGNVFAVAVSYFKALHTPTNELL 74
DB 12 SCPRFVNKLITSSHQPLFSCPDNFGYDMSHDYPLFGNIVINVSISHFQLHSPTNELL 71
QY 75 SLALADMFGLVLPSTIRSVSCWFGDELCRLHTYLTLFELCSIFHLCSIDRHC 134
DB 72 SNAITDFLLGFVIMPIRISRVSCWTFEGDECFKHTSTFIMRLTISIFHLCSIAIDRY 131
QY 135 AICDPLLYPSKFTVRAALRYIILAGWGPAPAYTSLFLYTDVETRLSQMLEMPVSCQL 194
DB 132 ACYCPPLHYTKMTNSTIKQLARCVSPALFSGVLSEL DVGMSQSYKILVACFMFCAL 191
QY 195 LNKFKGMLNF-PLFVPCILMISLVKIFVATROAQ:TTLSKSLAGAA-----KHE 247
DB 192 TENKFGTLFTTCFTFPGSINVGIGIKTIFYSKOHARV:SHNPETKGAVKKHLSKKD 251
QY 248 RRAKTLGIVGIGIYLLCMLPFTIDTWDSLHLHFTPLPLVDIPMFAYFNSACNPIIYV 307
DB 252 RRAKTLGIVGIGIYLLCMLPFLAVLIDRYLDTYLTIL:DLVWLRFTNSTCNPLIHGF 311
QY 308 STOWERRALKLTLISQFVSPQRTVDLYOE 337
DB 312 FNMFEOKAFKRYIVSGIKIFSSHSETANLPE 341

RESULT 5
US-09-555-313B-4
; Sequence 4, Application US/09555313B
; Patent No. 6506580
; GENERAL INFORMATION:
; APPLICANT: FICSHMEISTER, Rudolph et al.
; TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
; FILE REFERENCE: P067620S00/BAS
; CURRENT APPLICATION NUMBER: US/09/555,313B
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: FR 97/15037
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-313B-4

Query Match      25.5%; Score 455.5; DB 4; Length 360;
Best Local Similarity 34.5%; Pred. No. 4.4e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IOLVILYLT-CAAGMLTIIVGNVFAVAVSYFKALH-TPNELLSLALADMFGLVLP 90
DB 17 VERKVVLLTFLSTVIILMAIIGNLVAVAVCMDRQLRKIK:NYFLVSLAFNDLVSVLVMPF 76
QY 91 STIRSVSCWFGDFLCRLHTYLDLFCULTSIFHLCSIDRCAI-CDPLLYPSKFT-V 148
DB 91 STIRSVSCWFGDFLCRLHTYLDLFCULTSIFHLCSIDRCAI-CDPLLYPSKFT-V 148

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DB 77 GATELVODIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRYYAICCPLYVRNMTPL 136
QY 149 RVALARITLWG-VGVPAYTSLFL-----YTDVETR-LSQMLEMPVSCQLLNK 198
DB 137 RIAL--MLGGCWVIFPFISFLPMOGMNNIGIIDLEKRFKFNONSSTYCV----PMVK 190
QY 199 FWG-WLNFPLEFVPCILMISLVKIFVATROAQ:TTLSKSLAGAAKHE----- 248
DB 191 PVAITCSVAFAFIPFLMAYRIYVTAKEHAHQ:OMLOR--AGASSSRQSDAQHST 248
QY 249 -----KAKTIGIVGIGIYLLCMLPFTIDTWDSLHLHFTPLPLVDIPMFAYFNSACN 301
DB 249 HRRTETFKAKTLCIIMGFCICMAPEFVTNIVDPIDYVPGQVTAFLMIGYINSGLN 308
QY 302 PIIVFVSOMFRKALKTL 320
DB 309 PFLYAFLNKSFRAFLIIL 327

RESULT 6
US-09-555-313B-24
; Sequence 24, Application US/09555313B
; Patent No. 6506580
; GENERAL INFORMATION:
; APPLICANT: FICSHMEISTER, Rudolph et al.
; TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
; FILE REFERENCE: P067620S00/BAS
; CURRENT APPLICATION NUMBER: US/09/555,313B
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: FR 97/15037
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-313B-24

Query Match      25.5%; Score 455.5; DB 4; Length 380;
Best Local Similarity 34.5%; Pred. No. 4.6e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IOLVILYLT-CAAGMLTIIVGNVFAVAVSYFKALH-TPNELLSLALADMFGLVLP 90
DB 17 VERKVVLLTFLSTVIILMAIIGNLVAVAVCMDRQLRKIKTYFIVSLAFADLVSVLVMPF 76
QY 91 STIRSVSCWFGDFLCRLHTYLDLFCULTSIFHLCSIDRCAI-CDPLLYPSKFT-V 148
DB 77 GATELVODIWIYGEVFCVLTSLDVLTTASIFHLCCISLDRYYAICCPLYVRNMTPL 136
QY 149 RVALARITLWG-VGVPAYTSLFL-----YTDVETR-LSQMLEMPVSCQLLNK 198
DB 137 RIAL--MLGGCWVIFPFISFLPMOGMNNIGIIDLEKRFKFNONSSTYCV----PMVK 190
QY 199 FWG-WLNFPLEFVPCILMISLVKIFVATROAQ:TTLSKSLAGAAKHE----- 248
DB 191 PVAITCSVAFAFIPFLMAYRIYVTAKEHAHQ:OMLOR--AGASSSRQSDAQHST 248
QY 249 -----KAKTIGIVGIGIYLLCMLPFTIDTWDSLHLHFTPLPLVDIPMFAYFNSACN 301
DB 249 HRRTETFKAKTLCIIMGFCICMAPEFVTNIVDPIDYVPGQVTAFLMIGYINSGLN 308
QY 302 PIIVFVSOMFRKALKTL 320
DB 309 PFLYAFLNKSFRAFLIIL 327

RESULT 7
US-08-446-822-8
; Sequence 8, Application US/08446822
; Patent No. 5766879

```

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;; GENERAL INFORMATION:
;; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
;; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: COOPER & DUNHAM
;; STREET: 30 ROCKEFELLER PLAZA
;; CITY: NEW YORK
;; STATE: NEW YORK
;; ZIP: 10112
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,822
;; FILING DATE: June 1, 1995
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: White, P., John
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPM/NAT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 278-0400
;; TELEFAX: (212) 391-0525
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 388 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-446-822-8

Query Match      25.5%; Score 455.5; DB 1; Length 388;
Best Local Similarity 34.5%; Pred. No. 4.7e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVIVLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNPLLSLALADMFGLVLP 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 17 VEKVLLFTLSTVILMALGNLWVAACMDROLKIKTYFIYSLAPADLVSVLP 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 STIRSVESCMFEGDGLRLHTYLDLTLCTLSIFHLCTSIDRHCAI-CDPLLYPSKFT-V 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 GATLVODIWIYGEVFLVRSLOVLLTTASIFHLCCISIDRYAICQPLVYRNKMTPL 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 RVALRYILIAG-WGVPAAVTSIFL-----YTDVETR-LSQMLEMPVCGSCOLLINK 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 RIAL--MGGCWVLPFTISFLPIMGWNNIGIILIERKNONSNTYCV----FWYVK 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 FWG-WLNEPFEVPCLIWISLYKIFVAVTRQAOITTLSSLAGAKHER----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 PYATIGSVAVFIYFPLWLVAVRYRYAKHAHQIQMLQR--AGASESHPQSADQST 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 -----KAATLGIIVGIIYLLCWLPTIDTMVDSLHFTTPPLVDFITFAVNSACN 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 HRMRTETKAATLGIIMGCFCICWAPFEVTVIYDPIDYVPGQVWTAFLWLGINSGLN 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 PIIVFSYQMPFRKALKLTL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 PFLYAFLNKSFRRAPLITL 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-328-314-8
; Sequence 8, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinschank, Richard L.
```

```
;; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
;; FILE REFERENCE: 42667-A2-PCT-US
;; CURRENT APPLICATION NUMBER: US/09/328,314
;; CURRENT FILING DATE: 1998-04-03
;; EARLIER APPLICATION NUMBER: 08/446,822
;; EARLIER FILING DATE: 1995-07-31
;; EARLIER APPLICATION NUMBER: PCT/US93/12586
;; EARLIER FILING DATE: 1993-12-22
;; EARLIER APPLICATION NUMBER: 07/996,772
;; EARLIER FILING DATE: 1992-12-24
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 388
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-328-314-8

Query Match      25.5%; Score 455.5; DB 4; Length 388;
Best Local Similarity 34.5%; Pred. No. 4.7e-31;
Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVIVLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNPLLSLALADMFGLVLP 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 17 VEKVLLFTLSTVILMALGNLWVAACMDROLKIKTYFIYSLAPADLVSVLP 76
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 STIRSVESCMFEGDGLRLHTYLDLTLCTLSIFHLCTSIDRHCAI-CDPLLYPSKFT-V 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 GATLVODIWIYGEVFLVRSLOVLLTTASIFHLCCISIDRYAICQPLVYRNKMTPL 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 RVALRYILIAG-WGVPAAVTSIFL-----YTDVETR-LSQMLEMPVCGSCOLLINK 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 RIAL--MGGCWVLPFTISFLPIMGWNNIGIILIERKNONSNTYCV----FWYVK 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 FWG-WLNEPFEVPCLIWISLYKIFVAVTRQAOITTLSSLAGAKHER----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 PYATIGSVAVFIYFPLWLVAVRYRYAKHAHQIQMLQR--AGASESHPQSADQST 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 -----KAATLGIIVGIIYLLCWLPTIDTMVDSLHFTTPPLVDFITFAVNSACN 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 HRMRTETKAATLGIIMGCFCICWAPFEVTVIYDPIDYVPGQVWTAFLWLGINSGLN 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 PIIVFSYQMPFRKALKLTL 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 PFLYAFLNKSFRRAPLITL 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
PCT-US93-12586-8
; Sequence 8, Application PC/TUS9312586
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
```

REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US93-12586-8

Query Match 25.5%; Score 455.5; DB 5; Length 388;
 Best local Similarity 34.5%; Pred. No. 4.7e-31;
 Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVLYLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNELLISLADLMFLGLVLP 90
 DB 17 VERKVLTLFTSTVILMAIIIGNLVMVAVCDROLRIKTNCFIVSLAFADLVSVLWMP 76
 QY 91 STIRVESCWFEDFCLRLHTYDITLFCLSIFHLCSIRHCAI-CDELYPSKFT-V 148
 DB 77 GALELVODIMWYGEVCLVFTSLDVLITTAISPHLCISIKRYAICCPPLYVRNKMTP 136
 QY 149 RVALRYTLAG-WGVPAAYTSFL------YTDVETR-LSQWLEMPGVSCOLLNK 198
 DB 137 RIAL-MLGGCWYIPFISFLPMQGMNIGITLIEKRKNQNSSTYCV-PMVKN 190
 QY 199 FNG-WLNFPLFVPCCLIMISLYKIFVATROAQOITTLSSLAGAKHER----- 248
 DB 191 PVAITCSVAFAFYPLFLMVLAYRYIVTAKENHQIOMQR--AGASSESRPSADQHS 248
 QY 249 -----KAKTIGIVAGIYLLCWLPFTIDTMDLSLHFTTPPLVDFIWFAYFNSACN 301
 DB 249 HNRRTETKAKTKITIMGCFCICMAFPFVNIYDPIDYTPQVWTAFLMGLYINSGLN 308
 QY 302 PIIVFYSQWFRKAKLT 320
 DB 309 PFLYAFLNKSFRAFLIIL 327

RESULT 10
 US-09-555-313B-2
 ; Sequence 2, Application US/09555313B
 ; Patent No. 6506580
 ; GENERAL INFORMATION:
 ; APPLICANT: FICSHMEISTER, Rudolph et al.
 ; TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor
 ; FILE OF INVENTION: 5-HT4 and uses thereof, in particular for screening
 ; FILE REFERENCE: P067620500/BAS
 ; CURRENT APPLICATION NUMBER: US/09/555,313B
 ; CURRENT FILING DATE: 2002-08-13
 ; PRIOR APPLICATION NUMBER: FR 97/15037
 ; PRIOR FILING DATE: 1997-11-28
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 760
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-555-313B-2

Query Match 25.5%; Score 455.5; DB 4; Length 760;
 Best local Similarity 34.5%; Pred. No. 9.6e-31;
 Matches 110; Conservative 59; Mismatches 111; Indels 39; Gaps 12;

QY 33 IQLVLYLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNELLISLADLMFLGLVLP 90
 DB 17 VERKVLTLFTSTVILMAIIIGNLVMVAVCDROLRIKTNCFIVSLAFADLVSVLWMP 76
 QY 91 STIRVESCWFEDFCLRLHTYDITLFCLSIFHLCSIRHCAI-CDELYPSKFT-V 148

DB 77 GALELVODIMWYGEVCLVFTSLDVLITTAISPHLCISIDRYAICCPPLYVRNKMTP 136
 QY 149 RVALRYTLAG-WGVPAAYTSFL------YTDVETR-LSQWLEMPGVSCOLLNK 198
 DB 137 RIAL-MLGGCWYIPFISFLPMQGMNIGITLIEKRKNQNSSTYCV-PMVKN 190
 QY 199 FNG-WLNFPLFVPCCLIMISLYKIFVATROAQOITTLSSLAGAKHER----- 248
 DB 191 PVAITCSVAFAFYPLFLMVLAYRYIVTAKENHQIOMQR--AGASSESRPSADQHS 248
 QY 249 -----KAKTIGIVAGIYLLCWLPFTIDTMDLSLHFTTPPLVDFIWFAYFNSACN 301
 DB 249 HNRRTETKAKTKITIMGCFCICMAFPFVNIYDPIDYTPQVWTAFLMGLYINSGLN 308
 QY 302 PIIVFYSQWFRKAKLT 320
 DB 309 PFLYAFLNKSFRAFLIIL 327

RESULT 11
 US-07-996-772A-2
 ; Sequence 2, Application US/07996772A
 ; Patent No. 5472866
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe
 ; APPLICANT: Hartig, Paul R.
 ; APPLICANT: Branchek, Theresa A.
 ; APPLICANT: Weinschenk, Richard L.
 ; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN
 ; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM
 ; STREET: 30 ROCKEFELLER PLAZA
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/996,772A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, P., John
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 977-9550
 ; TELEFAX: (212) 664-0525
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 387 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-996-772A-2

Query Match 25.0%; Score 446.5; DB 1; Length 387;
 Best local Similarity 33.1%; Pred. No. 2.7e-30;
 Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

QY 33 IQLVLYLT-CAAGMLIIVGNVFAVAVSYFKALH-TPTNELLISLADLMFLGLVLP 90
 DB 17 VERKVLTLFTSTVILMAIIIGNLVMVAVCDROLRIKTNCFIVSLAFADLVSVLWMP 76
 QY 91 STIRVESCWFEDFCLRLHTYDITLFCLSIFHLCSIRHCAI-CDELYPSKFT-V 148
 DB 77 GALELVODIMWYGEVCLVFTSLDVLITTAISPHLCISIDRYAICCPPLYVRNKMTP 136


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; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12586
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-12586-2

Query Match      25.0%; Score 446.5; DB 5; Length 387;
Best Local Similarity 33.1%; Pred. No. 2.7e-30;
Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

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Db 17 VERVVLLTFPAMVILMAIIGNLLMVAVACHDRLRIKIKY(FVLSAFADLVSVLVNAF 76
QY 91 STIRSVESCFPGDFLCRLHTYVDTLFCLSIFHLCSIDRHCAL-CDPLVPSKFT-V 148
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 77 GATEIVQDIMEFGEMCLVNTSIDVLLTTSIFHLCSIDRYALCCOCPVLRNKKMTP 136
QY 149 RVALRYILAG-WGVPAAYTSLF-----YTDVYETR-----LSQMLEMPCVG 190
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 137 RIAL--MLGGCWVIPMFISFLPIMGWNNIGIVDIEKRKFNNNSSTFCVFNKRYAI 194
QY 191 SCOLLNKEFGWLNFLFEPFCLIMISLVKIFVAVTRONQITTLKSLAGAAKHER-- 248
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 195 TCSVV-----AFYIPFLMLAVAYRYITVTAKEHQIOMLOR--AGATSESRPQ 241
QY 249 -----KAKTLGIIVGIVLLCWLPTFTIDTVNDSLHFTTPPLVDFDIPIWFA 294
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 242 TADQHSTHRMRTETKAKATLCVIMGCFQMAFFVTNIVDPIDYVPEKVTATFLMG 301
QY 295 YFNSACNPITIVPSYQMFRRALKLTL 320
Db 302 YINSGINPFLYAFLNKSFRRALITL 327

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; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/328,314
; CURRENT FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: 08/446,822
; EARLIER FILING DATE: 1995-07-31
; EARLIER APPLICATION NUMBER: PCT/US93/12586
; EARLIER FILING DATE: 1993-12-22
; EARLIER APPLICATION NUMBER: 07/996,772
; EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-328-314-4

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Query Match      25.0%; Score 446.5; DB 4; Length 406;
Best Local Similarity 33.1%; Pred. No. 2.9e-30;
Matches 108; Conservative 55; Mismatches 110; Indels 53; Gaps 11;

QY 33 IOVLVILT-CAAGMLTIIVGNVFAVAVSYFKALH-TPTNFIILSLADMFGLVLP 90
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 17 VERVVLLTFPAMVILMAIIGNLLMVAVACHDRLRIKIKY(FVLSAFADLVSVLVNAF 76
QY 91 STIRSVESCFPGDFLCRLHTYVDTLFCLSIFHLCSIDRHCAL-CDPLVPSKFT-V 148
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 77 GATEIVQDIMEFGEMCLVNTSIDVLLTTSIFHLCSIDRYALCCOCPVLRNKKMTP 136
QY 149 RVALRYILAG-WGVPAAYTSLF-----YTDVYETR-----LSQMLEMPCVG 190
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 137 RIAL--MLGGCWVIPMFISFLPIMGWNNIGIVDIEKRKFNNNSSTFCVFNKRYAI 194
QY 191 SCOLLNKEFGWLNFLFEPFCLIMISLVKIFVAVTRONQITTLKSLAGAAKHER-- 248
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 195 TCSVV-----AFYIPFLMLAVAYRYITVTAKEHQIOMLOR--AGATSESRPQ 241
QY 249 -----KAKTLGIIVGIVLLCWLPTFTIDTVNDSLHFTTPPLVDFDIPIWFA 294
   |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 242 TADQHSTHRMRTETKAKATLCVIMGCFQMAFFVTNIVDPIDYVPEKVTATFLMG 301
QY 295 YFNSACNPITIVPSYQMFRRALKLTL 320
Db 302 YINSGINPFLYAFLNKSFRRALITL 327

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Search completed: August 26, 2003, 14:26:21
Job time : 22 secs

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RESULT 15
US-09-328-314-4
; Sequence 4, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinsbank, Richard L.

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